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Vaccines are non-toxic and antigenic to wild type pneumolysin, making them useful in vaccination against pneumonia and associated
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15-DEC-1989; AU0539.
16-DEC-1988; AU-001989.
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pneumolysin; vaccine; pneumonia; meningitis; bacteriaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATON JC, HANSMAN DJ, BOULNOIS GJ, ANDREW PW, MITCHELL TJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a soluble variant of Streptolysin O (SLO) having no haemolytic activity. The variant SLO can specifically recognise wild-type anti-SLO antibodies (ASO) but has no haemolytic activity. It can be used for the determination of previous and/or current infection by Streptococcus pyogenes. It enables ASO assays to become commercially viable and avoids the risk of handling haemony.
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03-AUG-1992; U06380.
30-AUG-1991; US-752/
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streptococcus pyogenes, ASO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptolysin O variants produced by recombinant DNA technology having no haemolytic activity and recognised by wild-type
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                                                                                                               257 vfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaaehnkvvtk 316
                                                                                                                                                      186 GEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQ 245
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  KVDMYEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLL
                                                                             VYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVTG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              active S. pyogenes wild-type SLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-752428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1416; DB 6;
Pred. No. 5.45e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 480;
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AC R33
AC R34
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wild type Streptolysin O
Claim 7; Fig 2; 60pp; English.
Claim 7; Fig 2; 60pp; English.
The sequence is that of a solible deriv. of Streptolysin O
with haemolytic properties which was obtd. from Streptococcus pyogenes
genomic library clone rSLO.3. It is useful in immunodiagnostic assays
which rely upon, e.g. the haemolytic properties of wild type
Streptolysin O. Recombinant Streptolysin O is obtd. more cheaply
than purified Streptolysin O obtd. from Streptococcus pyogenes.
             426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1992; U06398.
30-AUG-1991; US-752429.
(BECI ) BECKMAN INSTR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deriv. of streptolysin O with haemolytic activity immuno-diagnostic assays which rely on haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q38286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes. W09305156-A.
                                                                                                                                                                                                                                                                306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams CW, Wang EY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble streptolysin O variant.
Recombinant; haemolytic activity; immunodiagnostic activity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R33841;
08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                       257 vfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaaehnkvvtk 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AVNDLLAKWHQDYGQVNNVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            377 shqqayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgansrnirima 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 vtdrtypaalglankgftenkpdavvtkrnpqkihidlpgmgdkat-vevndptyanvst 136
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                                              sectglawewwrkviderdvklskeinvnisgstlsp 473
                                                                                                                                                                                                                                      KVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLL
                                                                                                            DHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI 425
                                                                                                                                                                       shqqayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgansrnirima 436
                                                                                                                                                                                                                                                                                          dfdvirnvikdnatfsrknpaypisytsvflknnkiagvnnrteyvettsteytsgkinl
   RECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP
                                                                                                                                                                                                                                                                                                                                                               VYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aldnlvngwhdnysggntlpartqytesmvysksqieaalnvnskildgtlgidfksisk 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQ 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNDFILAMNYDKKKLLTHQGESIENRFxKEGNQLPDEFVVxERKKRSLSTNTSDIXVTAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93-100980/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rectglawewwrkviderdvklskeinvnisgstlsp 473
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Similarity 41.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1398; DB 6; pred. No. 2.13e-109; 104; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480
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462
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Streptococcus pyogenes.

cleavage_site

Location/Qualifiers 33..34

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RESULT
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DT 22
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DE P1
KW S1
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                                 Bacteriophage lambda PL promoter - streptolysin O (SLO) fusion protein of plasmid pMK306. Streptolysin O; SLO; protease; bacteriophage lambda; ds.
                                                                  R06000 standard; protein; 371
R06000;
22-NOV-1990 (first entry)
Bacteriophage lambda PL promot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q10320.

Deriv. of thiol-activated protein streptolysin 0 - contg. no cysteine amino acid but retaining cytolytic activity, used for detecting antibodies in samples Disclosure; Fig 2; 9pp; English.

The SLO derivative contains no cysteine residues, with cytolytic activity giving resistance to inactivation by oxidation or thiol groups. Abs raised to the SLO may be used in the dection and diagnosis of Streptococcus pyogenes infection.
                                                                                                                                                                                     426
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                                                                                                                                                                                                                                                                                                                                                                                            348 vfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaaehnkvvtk 407
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WPI; 91-024598/04.
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04-JAN-1989;
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Streptolysin O derivative.
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                                                                                                                                                                                                                                                                                                                                                                                                                           186 GEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 gekkvmiaaykqifytvsanlpnnpadvfdksvtfkelgrkgvsneapplfvsnvaygrt 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 aidnlvngwhdnysggntlpartqytesmvysksqieaalnvnskildgtlgidfksisk 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169 vtdrtypaalqlankgftenkpdavvtkrnpqkihidlpgmgdkat-vevndptyanvst 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 indkiyslnynelevlakngetienfvpkegvkkadkfivierkkkninttpvdisiids 168
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(PINK/) PINKNEY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KEHO/) KEHOE
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                                                                                                                                                                                                        reatglawewwrkviderdvklskeinvnisgstlsp 564
                                                                                                                                                                                                                                     DHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI
                                                                                                                                                                                                                                                                   shqqayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgansrnirima
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                                                                                                                                                                                                                                                                                                                     RECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190;
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Pred. No. 8.88e-109;
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   Query Match
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SIO derivative is epitopic to its wild type parent, used in detecting anti-SIO Abs, indicating presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA2003307-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              raising antibodies, purifying antibodies or detecting antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-toxic and non-cytolytic derivs. of streptolysin 0 - used for
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17-NOV-1989; 026008.
18-NOV-1988; GB-027038.
17-NOV-1989; GB-026008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEHO/) KEHOE M.
of meningitis of meningitis 130pp; English. Claim 11; Page 53; 130pp; English. The sequence is that of the polypeptide encoded by a region isolated from S. pneumoniae which shows homology to pneumolysin. The protein, or agonists of it, may be useful as an antibacterial for
                                                                                                                                                     27-OCT-1997; U19226.
01-NOV-1996; US-029930.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas
                                                                              e.g.
                                                                                                                                                                                                                                                   WO9819689-A1.
                                                                                                                                                                                                                                                               Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae encoded polypeptide. coding region; ORF; open reading frame; antibacterial;
                                                                                                                                                                                                                                                                                                                                           W60952 standard; Protein; W60952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 PSNSSVRGAVNDLLAKWHODYGOVNNVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLD 177
                                                                                            New isolated nucleic acids from
                                                                                                            N-PSDB; V37352
                                                                                                                                                                                                                                                                               infection; prevention; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
                                                                                                                                                                                                                                   14-MAY-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
                                                                                                                                                                                                                                                                                                                                                                                                                    418 VRNLSVKIRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                     320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
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                                                                                                                                                                                                                                                                                                                            3-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 idfksiskgekkvmiaaykqifytvsanlpnnpadvfdksvtfkelqrkgvsneapplfv 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snvaygrtvfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaa 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aanpllvgvsakpvngwhdnyspgntlpartqytesmvysksqieaalnvnskildgtlg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90-217310/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ehnkvvtkdfdvirnvikdnatfsrknpaypisytsvflknnkiagvnnrteyvettste 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDFNSVHSGEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SXVAYGRQVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                srnirimarectglawewwrkviderdvklskeinvnisgstlsp 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ytsgkinlshqgayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgan 319
                                                                                                                         98-286586/25.
                                                                              for identifying anti-bacterial(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                           Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label=Lambda N promoter -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.9%;
                                                                                                                                                                                                                                                                                                                                                           113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1097; DB 1;
Pred. No. 7.61e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 122;
                                                                                               Streptococcus
                                                                                 for
                                                                                 treatment
                                                                                 pneumoniae
eatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 371;
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                                                                                                                                                             80
                                                                                 prevention
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                                                                                                 useful,
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                                            밁
                                                                                                                                                                                                            printernalises polynucleotide (PN) into endosome, then lyses endosome in the respective present peptide is a listeriolysin o (LLO) haemolytic domain complex present peptide is a listeriolysin o (LLO) haemolytic domain complex present peptide is a listeriolysin o (LLO) haemolytic domain complex present peptide in the LLO coding sequence in a coluble molecular complex, for the specific targetting of a coluble molecular complex, for the specific targetting of a collynucleotide (PN) to a cell. The complex comprises a PN, a complex comprises a PN, a confict of the cell specific binding carrier comprising a PN binding agent and a cell specific binding carrier comprising a PN binding agent and a cell and is contennalised into an endosome, and a bacterial component (i.e. the coll plus LLO HD fragment), which lyses the endosome to release the pN into cell's cytoplasm. The complex can be used therapeutically component in vivo, ex vivo or in vitro delivery of a PN to a confirmal component in the complex can be used therapeutically component in the complex can be used therapeutically component in vivo, ex vivo or in vitro delivery of a PN to a confirmal component in the complex can be used therapeutically component in vivo, ex vivo or in vitro delivery of a PN to a confirmal component in vivo.
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Best Local :
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                                                                                         Matches
                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial gene expression. Detecting a sequence encoding the protein can be used diagnostically, e.g. to detect a mutation for serveryping or classifying infectious agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeriolysin O haemolytic domain peptide.

Listeriolysin O; haemolytic; domain; streptolysin O; pneumolysin; soluble molecular complex; specific; targetted; polynacleotide; endosome lysis; bacterial component; cytoplasm; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /T 8
R88135 standard; peptide; 
R88135;
29-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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27-JUN-1995; U08091.
29-JUN-1994; US-267710.
07-JUN-1995; US-484009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
W09600792-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carmichael E, WPI; 96-07750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble molecular complex for specific targetting of PN to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in vivo; ex vivo; in vitro; delivery; cell specific;
                                                                                                                                                                           Sequence
                                                                                                                                                                                                specific cell
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Local Similarity 43.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 rnlrvkiekktgllwnrwgtiyenrpilagphrkithwgttlnskvsdddv 112
427 ECTGLAWEWWR 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 kdktliighsgayiarysitweevpvdkdgngvvrshswegngrngtagfvlnlpikenm 61
                                          1 ectglawewwr 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNLSVKIRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQV-EDKV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNV 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96-077502/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                           3.5%;
Similarity 100.0%;
                                                                                         11;
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                                                                                                                                                                      11 AA;
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                                                                                    Conservative
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Pred. No. 7.
32; Mismatc
                                                                                      Pred.
                                                                                                                Score 112;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .90e-20;
ches 30;
                                                                                         Db
.96e+00;
0;
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                                                                                                                                          DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang
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                                                                                                                                     Length 11;
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Best Local
                        07-AUG-1997.
01-FEB-1996; 003649.
01-FEB-1996; DE-003649.
(LUBI/) LUBITZ W.
(SLEY/) SLEYTR U.
                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus stearothermophilus S-layer protein sbs-A. S-layer; sbs-A; vaccine; adjuvant; carrier; hybridisation assay;
                                                                                                                                                                                  DE19603649-A1.
                                                                                                                                                                                                                                                                                                                                                                          molecular spinning nozzle; molecular laser
                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W22862 standard; Protein; 1228 AA.
                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                             Bacillus
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27 -OCT 1997; U19226.
27 - NOV 1996; US-029930.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OI meningitis
Claim 11; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acids from Streptococcus pneumoniae - useful, e.g. for identifying anti-bacterial(s) for treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae W09819689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae encoded polypeptide. coding region; ORF; open reading frame; antibacterial; infection; prevention; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V37371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 GALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLAS-SDSFLQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 dystnaifdhhgqakvslfakeagvlag-ltvfqrvftlfdaevtfqnphqfkdgdrlts 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 3.3%;
Local Similarity 21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gdl-vl-eiig-svrslltcervalnflqhlsgiasmtaayve 136
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                                                                                                                                                                                                                                                                                                                                                       stearothermophilus
   Lubitz W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 71-72; 130pp;
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                                                                                                                                                                                                                                                        /label= sig_peptide
                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                          /label=
Sleytr U;
                                                                                                                                                                                                                                      .1228
                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 108; DB 33;
Pred. No. 1.10e+01;
35; Mismatches 4(
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RESULT
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PT epitope(s), as present sequence is the Bacillus stearothermophilus pv72
PT epitope(s), as an universal sequence in its membrane. Other uses of adjuvants, particularly when they include a bacterial ghost that adjuvants additional epitopes in its membrane. Other uses of the combinant sbs-A, depending on the nature of the inserted peptide, are as an universal carrier for biotinylated reactants for use in a control in the immunity of the insert is streptavidin), and to induce immune responses (epitopes), as a reagent for removing cytokine or toxin from serum (antigenic epitopes), as a molecular of laser (in-if-paraea)
                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                           Disclosure; Page 6-7; 12pp; German.

The claimed signal peptide encoding sequence (see tag e of T08695) is pref. operably linked at the 3' end to a protein encoding sequence. The protein is pref. the S-layer protein (see tag f of T08695). At the 5' end, the signal peptide encoding sequence is
                                                                                  given in T08696.
Sequence 1228 AA;
                                                                                                                                                                                                                                                          S-layer protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-layer protein encoded by sbsA gene.
sbsA gene; S-layer; cell surface layer; expression.
Bacillus stearothermophilus.
                                                                                                                                                                                                                                                  Nucleic acid encoding signal peptide of Bacillus stearothermophilus S-layer protein - which has a lysine content of at least 10 per
                                                                                                                                                                                                                                                                                                    N-PSDB; T08695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R77673 standard; Protein; 1228 R77673;
                                                                                                                                                                                                                                                                                                                                                                             19-JUL-1994; 425527.
19-JUL-1994; DE-425527
                                                                                                                                                                                                                                                                                                                                                                                                                                      DE4425527-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
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                                                                                                                                                                                                                                                                                                                                       Lubitz W;
                                                                                                                                                                                                                                                                                                                                                   (VOGE-) VOGELBUSCH GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-1996
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N-PSDB; T75487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 S-RETADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG
  3.3%;
Local Similarity 23.5%;
les 39; Conser.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 nipfalntadvslstdgktitvdastpfennteykvvvkgikdkng 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 yditv-amkar-ev-qdavkagnldkakaavdqinqylpkvtdafktelt-evakkalda 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 -EAAFEALIKGVKVÄPQTEWKQI-LDNTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 deaaltpkvesvs-aintqnkaveltavpvngt-lklqlsaaanedtvnvntvriykvdg 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQVYLKLETTSxSxEV 259
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                                                                                                                                                                                                                                                                                                                  96-077933/09.
                                                                                                             linked to an expression control sequence, pref. the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity 23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                31..1228
/label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= sig_peptide
Score 107; DB 1/, Pred. No. 1.28e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 25;
Pred. No. 1.28e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
                                        Length 1228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1228;
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Matches

Indels 10;

10;

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Qy
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γg
                                          В
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                                                                                                                          Ъ
                                                                                                                                                                                                                                                                                                          This sequence is a H. pylori protein of unspecified function. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, infection or to identify H. pylori polypeptide binding compounds, is useful as potential H. pylori life cycle activators or inhibitors. The DNA and probes derived from it may be used for the identification of the pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies and the protein can be used in immunoassays to evaluate the abundance of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF continued for spificant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR complification for recombinant polypentide production, e.g., in E. coli
                                                                                                                                                                      Matches
                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection and for diagnosis of H. pylori infection (Claim 14; Page 571; 1145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-1996; US-625811.
02-APR-1996; US-758731.
25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
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06-DEC-1996; US-761318.
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N-PSDB; V24756.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9737044-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASTR
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                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                            amplification for recombinant polypeptide production,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 yditv-amkar-ev-qdavkagnldkakaavdqinqylpkvtdafktelt-evakkalda
                                          152 1 152
                                                                                    210
  270 V 270
                                                                                                                                                                                          Local
                                                                                                                          95 psslmrdsvsledskkr-lnaikdlifhknkaf-rqlqlklntplkal-veaqkdgefka 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pylori ORF 01ce11618orf11 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-RFTADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG
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                                                                                    PGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGRQVYLKLETTSXSXEVEAAFEALIKG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ASTRA AB.
A, Smith D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 188 AA
                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                         188 AA;
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                                                                                                                                                                    Conservative
                                                                                                                                                                                        3.1%;
                                                                                                                                                                      Pred.
20; !
                                                                                                                                                                                          Score 101; DB 29; Pred. No. 3.16e+01;
                                                                                                                                                                         Mismatches
                                                                                                                                                                           18;
                                                                                                                                                                                                                 Length 188;
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Claims 14.93; Page 730-731; 1145p; English.

CC This sequence is a H. pylori cellular protein.

CC The protein may be used in a vaccine to prevent or treat H. pylori compounds, or the protein may be used for the protein or to identify H. pylori polypeptide binding compounds, or the protein or to identify H. pylori polypeptide binding compounds, or useful as potential H. pylori life cycle activators or inhibitors. The condition of the pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies can distribution of H. pylori-specific antispens. The genomic sequence of the pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed cor or or for at least 180 nucleotides, and the predicted coding regions confidence development, the amino acid sequences predicted from various or vaccine development, the amino acid sequences predicted from various or compliments, Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR camplification for recombinant polypeptide production, e.g. in E. coli
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Best Local S
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WPI; 97-
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W55528 standard; Protein; 418
W55528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H. pylori ORF 29ge30321_24336712_f1_5 cellular protein. Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-1996;
25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-1998
                                                                                         H. pylori transporter protein, 06gpl1202orf7.

Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1996;
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                                                      Helicobacter pylori. W09640893-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
19-DEC-1996.
06-JUN-1996; U09122.
07-JUN-1995; US-487032.
                                                                                                                                                                                            W20753;
                                                                                                                                                                                                            л 14
W20753 standard; protein; 667 AA.
                                                                                                                                                                                                                                                                                                                                                                                          325 psslmrdsvsledskkr-lnaikdlifhknkaf-rqlqlklntplkal-veaqkdgefka 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nosts.
                                                                                                                                                                          16-JUL-1997 (first entry)
                                                                                                                                                                                                                                                                                                                             382 1 382
                                                                                                                                                                                                                                                                                                                                                                  270 V 270
                                                                                                                                                                                                                                                                                                                                                                                                                                         3.1%;
Similarity 32.8%;
20; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            418 AA;
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US-761318.
US-625811.
US-758731.
US-736905.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-738859
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101; DB 29; I
Pred. No. 3.16e+01;
20; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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prippeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter PS Claim 56; Page 1166-1167; 1481pp; English.

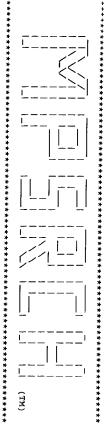
CC The present sequence is a Helicobacter pylori transporter protein. CC The protein may be used in a vaccine to prevent or treat H. pylori CC infection or to identify H. pylori polypeptide binding compounds, CC useful as potential H. pylori life cycle activators or inhibitors.

CC The genomic sequence of H. pylori (ATCC 55679) was determined from CC overlapping contigs generated by mechanically shearing the bacterial CC and the predicted coding regions defined by computer evaluation. To CC identify likely H. pylori antigens for vaccine development, the amino CC acid sequences predicted from various ORF were analysed for significant CC and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide Sequence 667 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKBP; heat shock protein; hsp90; chaperone protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               steroid hormone receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-1994 (first entry)
Rabbit HBI protein which binds hsp90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R41781 standard; Protein; 458 AA. R41781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rotamase activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T68006
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WPI; 97-052306/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 ISXVAYGRQVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTEVK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity 26.9%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith D,
               /note= "antiparallel beta-pleated sheet"
                                                                                                 /note= "antiparallel beta-pleated sheet"
53..61
                                                                                                                                                /note= "CAM"
33..39
                                                                                                                                                                                             /note= "globular domain'
373..458
                                                                                                                                                                                                                                                                            identity with FKBP and comprises 4 zones of insertions or deletions"
                                                                                                                                                                                                                                                                                                                                                          /labe1
                                                                                                                                                                                                                                                                                                                                                                                      /note= "immunophilin domain; has 49 per cent
identity with FKBP without introducing
insertions or deletions into the sequence"
139..148
                                    /label- A5
                                                              /note= "antiparallel beta-pleated sheet"
                                                                                    'label= A4
                                                                                                                                 'label= A1
                                                                                                                                                                             'label= C-terminal
                                                                                                                                                                                                                                                            'labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                            labe1=
                                                                                                                                                                                                                                                                                                                                           label-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppressor; FK506; binding protein;
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Pred. No. 3.16e+01
15; Mismatches 2
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           New protein forming complex with heat shock protein - also binding immuno-suppressors, etc., and corresp. nucleic acid, antibodies etc., useful e.g. for detecting tumours, treating auto-immune disease, etc.

Claim 1; Fig 1; 43pp; French.

The HBI protein is able to complex chaperone protein hsp90, even when the chaperone protein is part of a hetero-oligomer with other proteins. Hsp90 can bind to steroid hormone receptors, vitamin D, and Tyrosine Kinases of viral oncogenes; HBI is thus useful for the
                                                                                                                                                                 Baulieu E, Callebaur ,
Mornon J, Radanyi C, Renoir M;
                                                                                                                                                   N-PSDB; Q48515.
                                                                                                                                                                                                                                 04-MAR-1993;
04-MAR-1992;
                                                                                                                                                                                             (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. Baulieu E, Callebaut I, Chambraud B, Lebeau
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362..371
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/note= "antiparallel beta-pleated sheet"
243..252
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217..2
                                                                                                                                                                                                                                                                                        /note= "used to generate polyclonal antibodies"
                                                                                                                                                                                                                                                                                                                        /note=_"site of interaction with calmodulin"
                                                                                                                                                                                                                                                                                                                                                     /note= "antiparallel beta-pleated sheet"
                                                                                                                                                                                                                                                                                                                                                                              /label= A3
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/note= "antiparallel beta-pleated sheet"
289..297
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/note= "supplementary
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/label= beta
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 3 13:10:39 1999; MasPar time 20.83 Seconds 905.977 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

>US-09-120-044-3-COPY (1-471) from devil20044.pep 3234 1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 50.326; Variance 110.458; scale 0.456

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

110 1111 1111 1111 1111 1111 1111 1111	7654321	Result
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tanabin - African cla	₹	UL37 protein - human	cation efflux system	valinetRNA ligase (hypothetical protein	hypothetical protein	hypothetical 58.2 kD	arginine decarboxylas	glycine hydroxymethyl	hypothetical protein	probable aminotransfe	hypothetical protein	cell division inhibit	£		de		flagellin H-1 - Salmo	ac	Õ	hypothetical protein
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Db 61 SVTATN	Db 1 MANKAV Qy 1 MANKAV	Query Match Best Local Similarity Matches 461; Conse	2-471 SUMMARY	##molecule_type ##residues ##cross-referen CLASSIFICATION #sup	#accession	#cross-refere	#title	#autnors	REFERENCE	##residues	#accession	#cross-refere		#ťitle	#journal	#authors	ACCESSIONS	TITLE ORGANISM DATE	RESULT 1 ENTRY
SVTATNDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSN 120 	MANKAVNDFILAMNYDKKKLLTHQGESIENRFIKEGNQLPDEFVVIERKKRSLSTNTSDI 60 	h .99.9%; Score 3232; DB 2; Length 471; .Similarity 97.9%; Pred. No. 0.00e+00; Indels 0; Gaps 0;	<pre>#product pneumolysin #status predicted #label MAT #length 471 #molecular-weight 52899 #checksum 8274</pre>	##molecule_type DNA ##rosidues 1-471 ##label MIT ##cross-references EMBL:X52474; NID:g47403; PID:g47404 ##CICATION #superfamily dipeptide transport protein E	S12829 preliminary	Streptococcus pneumoniae types 1 and 2. cross-references MUID:90326546	Comparison of pneumolysin genes and proteins from	Mitchell, T.J.; Mendez, F.; Paton, J.C.; Andrew, P.W.; Boulnois, G.J. While the state of the sta	S12829	Type UNA 1-471 ##label WAL	A28568	sulinydryl-activated toxin of Streptococcus pneumoniae.	for pneumolysin, the	Molecular cloning, characterization, and complete nucleotide	Boulnois, G.J. Infect Immun /1987) 55:1184-1180	Walker, J.A.; Allen, R.L.; Falmagne, P.; Johnson, M.K.;	21-Aug-1996 A28568; S12829 A28568	pneumolysin - Streptococcus pneumoniae #formal_name Streptococcus pneumoniae 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change	A28568 #type complete

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ACCESSIONS
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                                                                                                                                                            ##residues 29-45 ##label TW2
##experimental_source ATCC 13124
                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-125,'EA',129-500 ##label TWE ##cross-references GB:M36704; NID:g144883; PID:g144884
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                                                                                                                                                                                      ##molecule_type protein
##residues 29-45 #
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##cross-references GB:M81080; NID:g144885; PID:g144886
#mote translation of the nucleotide sequence is not complete
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                                                                                                                                                                                                                                                                 Tweten, K.K.

Infect. Immun. (1988) 56:3228-3234
Cloning and expression in Escherichia coli of the perfringolysin O (theta-toxin) gene from Clostridium perfringence and characterization of the gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tweten, R.K.

Infect. Immun. (1988) 56:3235-3240

Nucleotide sequence of the gene for perfringolysin O

(theta-toxin) from Clostridium perfringens: significant homology with the genes for streptolysin O and pneumolysin.
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A43577; Shimizu, T.; Okabe, A.; Minami, J.; Hayashi, Infect. Immun. (1991) 59:137-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B43577 #type complete
perfringolysin O precursor - Clostridium perfringens
#formal_name Clostridium perfringens
03-Feb-1993 #sequence_revision 03-Mar-1993 #text_change
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Best Local Similarity 46.5%;
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                                        ##experimental_source strain EGD
##note this sequence is derived from a weakly hemolytic strain,
                                                                                                         ##residues
                                                                                                                                                                                                                                                                                                                                         ##cross-references GB:M24199;
                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type DNA
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                                                                                ##Cross-references EMBL:X15127; NID:g44106; PID:g44107
                                                                                                                      ##molecule_type DNA
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listeriolysin O precursor - Listeria monocytogenes
#formal_name Listeria monocytogenes
21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change
17-Mar-1999
                                                                                                                                                   S05306
                                                                                                                                                                                       Domann, E.; Chakraborty, T.
Nuclect Acids Res. (1989) 17:6406
Nucleotide sequence of the listeriolysin
monocytogenes serotype 1/2a strain.
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Infect. Immun. (1988) 56:766-772
Expression in Escherichia coli and sequence analysis of the
listeriolysin O determinant of Listeria monocytogenes.
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Geoffroy, C.; Gicquel-Sanzey, B.; Baquero, F.; Perez-Di
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Pred. No. 2.15e-270;
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                                                                                                                                                                                                                                                                                                                                         185 SGEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 NDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG
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                                                                                                                                                                                                                            GNLGDLRDILKKGATFNRETPGVPIAYTTNFLKDNELAVIKNNSEYIETTSKAYTDGKIN 420
                                                                                                                                                                                                                                                                                                         QVYLKLSTNSHSTKVKAAFDAAVSGKSVSGDVELTNIIKNSSFKAVIYGGSAKDEVQIID 360
                                                                                                                                                                                                                                                                                                                                                                      EGKMQEEVISFKQIYYNVNVNEPTRPSRFFGKAVTKEQLQALGVNAENPPAYISSVAYGR 300
                                                                                                                                                                                                                                                                                                                                                                                                         AVNDLLAKWHQDYGQVN-NVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
                                                                                                              AKECTGLAWEWWRTVIDDRNLPLVKNRNISIWGTTLYPKYSNKVDN 526
                                                                                                                                                                                                             GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL 364
                                                                                                                                                                                                                                                                           QVYLKLETTSxSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                               IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN 470
                                                                                                                                              LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
                                                                                                                                                                             IDHSGGYVAQFNISWDEVNYDPEGNEIVQHKNWSENNKSKLAHFTSSIYLPGNARNINVY 480
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Similarity 42.9%;
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Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtained by single amino acid substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Infect. Immun. (1987) 55:3225-3227
Identification of the structural gene encoding the
SH-activated hemolysin of Listeria monocytogenes:
listeriolysin O is homologous to streptolysin O and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label
#product listeriolysin O #status predicted #label
#length 529 #molecular-weight 58688 #checksum 719
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S24231 #t
listeriolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.7%; Score 1543; DB 2; I
larity 42.9%; Pred. No. 1.85e-259;
Conservative 117; Mismatches 148;
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##experimental_source strain 12067, serotype 4b
##note the nucleotide sequence was submitted to
Library, June 1991
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Similarity 42.7%;
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strain 12067
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
13-Sep-1998
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$22341 #type complete ivanolysin precursor - Listeria formal_name Listeria ivanovii 07-Apr-1994 #sequence_revision
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Pred. No. 4.06e-258;
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                                                                Listeria ivanovii
        07-Apr-1994
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21-Aug-1998

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#journal Biochim. Biophys. Acta (1992) 1130:81-84
#title Listeriolysin genes: complete sequence of ilo from Listeria
ivanovii and of lso from Listeria seeligeri.
#cross-references MUID:92182018
#accession S22341
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##residues 1-528 ##label HAS
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                                                  $22340 #type complete
seeligeriolysin - Listeria seeligeri
#formal_name Listeria seeligeri
22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change
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#length 528 #molecular-weight 58511 #checksum 6874
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ACCESSIONS
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#accession S22340
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##residues 1-501 ##label GEO
##cross-references GB:M62709; NID:g142472; PID:g142473
#length 501 #molecular-weight 55268 #chec
                                                       ##molecule_type DNA
##residence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 IDHSGGYVAQFNISWDEVSYDENGNEIKVHKKWGENYKSKLAHFTSSIYLPGNARNINIY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 QVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 ISSLTYPGALVKANRELVENQPNVLPVKRDSLTLSVDLPGMTKKDNKIFVKNPTKSNVNN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 INKYIWGLNYDKNSILVYQGEAVTNVPPKKGYKDGSEYIVVEKKKKGINQNNADISVINA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 45.7%;
Local Similarity 42.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNLGELRDILKKGSTYDRENPGVPISYTTNFLKDNDLAVVKNNSEYIETTSKSYTDGKIN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVYVKLSSSSHSNKVKTAFEAAMSGKSVKGDVELTNIIKNSSFKAVIYGGSAKEEVEIID 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVNDLLAKWHQDYGQVN-NVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVNTLVERWNDKYSKAYPNINAKIDYSDEMAYSESQLIAKFGTAFKAVNNSLNVNFEAIS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198;
                                                                                                                  A37858
                                                                                                                                                                          Geoffroy, C.; Mengaud, J.; Alouf, J.E.; Cossart, P.
J. Bacteriol. (1990) 172:7301-7305
Alveolysin, the thiol-activated toxin of Bacillus alvei, homologous to listeriolysin O, perfringolysin O, pneumolysin, and streptolysin O and contains a single
                                                                                                                                                                                                                                                                                                                         A37858 #type complete
alveolysin - Bacillus alvei
#formal_name Bacillus alvei
28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change
09-Sep-1997
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#length 530 #molecular-weight 59181 #c
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Biochim. Biophys. Acta (1922) 1130:81-84
Listeriolysin genes: complete sequence of ilo from Listeria
ivanovii and of lso from Listeria seeligeri.
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                                                                                                                                                        cysteine
                                                                                                                                 MUID: 91072294
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Pred. No. 8.14e-247;
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                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal
#title
                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane-damaging, thiol-activated toxins
#cross-references_MUID:88057628
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                                                                                                                                                                                                                                                                                                            ##residues 1-571 ##label KEH
##cross-references GB:M18638; NID:g153810; PID:g153811
## #length 571 #molecular-weight 63638 #chec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463
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                     228
                                                                                                      169
                                                                                                                                                                                    109 INDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIERKKKNINTTPVDISIIDS 168
                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                 ##status
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                                                               66
                                                                                                                                                                                                                                                 Local Similarity 41.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLLDHSG
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AIDNLVNOWHDNYSGGNTLPARTQYTESMYYSKSQIEAALNVNSKILDGTLGIDFKSISK
                                                               NDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG 125
                                                                                                    VTDRTYPAALQLANKGFTENKPDAVVTKRNPQKIHIDLPGMGDKAT-VEVNDPTYANVST 227
                                                                                                                                               VNDFILAMNYDKKKLLTHQGESIENRFxKEGNQLPDEFVVxERKKRSLSTNTSDIxVTAT 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Infect. Immun. (1987) 53:3440 5444 Nucleotide sequence of the Streptolysin O (SIO) gene: Structural homologies between SIO and other structural homologies between toxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               streptolysin o precursor - Streptococcus pyogenes
#formal_name Streptococcus pyogenes
28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                       A43507
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Infect. Immun. (1987) 55:3228-3232
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                                                                                                                                                                                                                                104; Mismatches 161;
                                                                                                                                                                                                                                                 Score 1408; DB 2; Length 571; Pred. No. 1.28e-233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-485 ##label RES
##cross-references GB:D21270; NID:g418066;
#length 485 #checksum 3782
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  305
                                                                                                                                                                                                    223
                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
                                        343
                                                                                                                                                            185
                                                                                                                                                                                                                                          125 GAVNDLLAKWHQDYGQVNNVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
                                                                                                                                                                                                                                                                                   163 GAVDDLVSTWNEKYSATHTLPARMQYTESMVYSKAQIASALNVNAKYLDNSLNIDFNAVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##status
                                                                                                                                                                                                                                                                                                                           65 TNDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                               44 SIDTGIGNLTYNNQEVLAVNGDKVESFVPKESINSNGKFVVVDVRKNHLQRHQSIFRLLD 103
                                                                                                                                                                                                                                                                                                                                                                                                         5 AVNDFILAMNYDKKKLLTHQGESIENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVTA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFVKLETSSKSNDVEAAFSAALKGTDVKTNGKYSDILENSSFTAVVLGGDAAEHNKVVTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECTGLAWEWWRTVYEXTDLPLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHQGAYVAQYEILWDEINYDDKGKEVITKRRWDNNWYSKTSPFSTVIPLGANSRNIRIMA
                                                                                                       TVYVKLETTSKSKDVQAAFKALLKNNSVETSGQYKDIFEESTFTÄVVLGGDÄKEHNKVVT 342
  GKVDMVEDLIQEGSRFTADHÞGLÞISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                      KDFNEIRNIIKDNAELSFKNPAYPISYTSTFLKDNATAAVHNNTDYIETTTTEYSSAKMT 402
                                                                              QVYLKLETTSxSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                                            SGEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGR
                                                                                                                                                                                                  NGEKKYMVAAYKQIFYTVSAELPNNPSDLFDNSVTFGELTRKGVSNSAPPVMVSNVAYGR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.18;
11 Similarity 39.58;
172; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yutsudo, T.; Okumura, K.; Iwasaki, M.; Hara, A.; Kakitani, S.; Minamide, W.; Igarashi, H.; Hinuma, Y.
Infect. Immun. (1994) 62:4000-4004
The gene encoding a new mitogenic factor in a Streptococcus pyogenes strain is a distributed only in group A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139863  #type fragment
hemolysin - Bacillus cereus (fragment)
#formal_name Bacillus cereus
19-Jul-1996  #sequence_revision 19-Jul-1996  #text_change
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##residnee
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                                                                                                                                                                                                                                                                                  ##cross-references EMBL:236907; NID:g535305; pj
#length 96 #molecular-weight 10471
                                                                                          64 ATNDSRLYPGALLVVDETLXENNPTLLAV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:236908; NID:g535307; PID:g535308
#length 112 #molecular-weight 12464 #checksum 9264
                                                                                                                          61 XAKAANISPGALLRAXQNLLDNNPTLISI 89
                                                                                                                                                                                                                                       Watch 6.6%;
Local Similarity 33.7%;
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 monoamine oxidase
                amine oxidase
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S47297
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#formal_name Streptococcus suis
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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suilysin - Streptococcus suis
#formal_name Streptococcus suis
06-Jan-1995 #sequence_revision (
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S47297
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se (flavin-containing) (EC
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                                                                                                                                                                                                                      Score 214; DB 2;
Pred. No. 3.28e-15;
23; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 464; DB 2; Length 112
Pred. No. 2.28e-57;
22; Mismatches 33; Indels
type
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Best Local
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                                                                                                                                                                                                #submission
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #cross-references MUID:89246344
#accession S03974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors
                                                                 ##experimental_source strain
                                                                                       ##cross-references EMBL: Z73307; NID:g1360550; MIPS:YLR135w
                                                                                                                               ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-527 ##label POW ##cross-references GB:X15609; NID:9523; PID:9524 FAD; flavoprotein; mitochondrion; oxi
                                                                                                                                                 ##molecule_type DNA
                                                                                                                                                                                                                                                                                 ##cross-references EMBL:X91258;
                                                                                                                                                                                                                                                                                                                         ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 GAYVAQYYITWNELSYDHQGKEVLTPKAWD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 IAYL-DYNNLWRTM--DNMGKEIPADAPWE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 VEDLIQEGSRFTADHPGLPISYTTSF-LRDNVVATFQNSTDYVETKVTAYRNGDLLLDHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 LETTSxSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVTGKVDM 309
                                                                                                                                                                                                                                                               ##experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 3.6%;
Local Similarity 19.3%;
hes 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 V-DYVDVGGAYVGPTQNRILRLSKQLGLETYKVNVNERLVHYVKGKTYPFRGAFPPVWNP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MESLQKTSDAGQMFDVVVIGGGISGLSAAK-LLAEHEVNVLVLEARERVGGRTYTVRNEH 59
                                                                                                                                                                          Delius, H.; Hebling, U. submitted to the Protein S64977
                                                                                                                                                                                                                                                                                                                                                           Delius, H. submitted to the EMBL Data Library, June 1995 36.8 kb of S.cerevisiae chromosome XII includ. PDC5, SLS1, PUT1 and tRNA-Asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein L3140

#formal_name Saccharomyces cerevisiae
29-Nov-1995 #sequence_revision 23-Feb-1996

05-Dec-1997_
  #length 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Powell, J.F.; Hsu, Y.P.P.; Weyler, W.; Chen, S.; Salach, Andrikopoulos, K.; Mallet, J.; Breakefield, X.O. Biochem. J. (1989) 259:407-413

The primary structure of bovine monoamine oxidase type A. Comparison with peptide sequences of bovine monoamine oxidase type B and other flavoenzymes.
                                                                                                                                                                                                                                                                                                                                                    S5932
                                                                                                                                                                                                                                                                                                                                                                                                                                                              S59313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S59327; S64977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S59327 #type complete
hypothetical protein YLR135w - yeast (Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #length
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28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerevisiae)
                                                                                                                                                                                                                                                             source strain S288C
                                                                                                                             1-748 ##label DEW
                                                                                                                                                                                                                                                           DNA
1-748 ##label DEL
--- השתר.: 291258; NID: 9995686; PID: 9995701
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#modified_site S-(8alpha-FAD)-cysteine (Cys) #status
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n 527 #mo
#molecular-weight 84361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 117; DB 2; Le
Pred. No. 1.18e-01;
42; Mismatches 73;
                                                                                                                                                                                              Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oxidoreductase
                                                                                                       PID:e245572; PID:g1360551;
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#checksum
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TITLE
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Best Local Similarity 26.3%;
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#start_codon TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #cross-references MUID:96337999
#accession F64461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##molecule_type DNA
##residues 1-218 ##label BUL
##cross-references GB:U67570; GB:L77117; NID:g1591929; PID:g1591933;
##cross-references TIGR:MJ1295; PID:g1511304
                                                                                                                                                                                                                                                                         213 V-FODTVTVEDLKORGISAE 231
                                                                                                                                                                                                                                                                                                                        127 PGFIDKETAENLKENDIFVE 146
                                                                                                                                                                                                                                                                                                                                                                 153 ITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHSGEKQIQIVNxKQIYYTVSVDAVKNPGD 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 YGQVNN-VPARXQY-EKI-T-AH-SMEQLKVK-FGSD-FEKTGNSLDI-DFNSVHS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              627 SQSMKELRQSLKTVGLKPMRTKVEIIQSLQTASQILSTANPDNKGEHGGVANF-SK-IEI 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               567 SEEEETEFDDQFCIADIQLVDSSKISTKDSTQNPTTSNDIIDTSAASSIASPEKFCEIMM 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 FDHLTELIEAFPDFLERIYTFEPIPLNELIEKLESAEPFVSQIDEMTIREWADVQG 740
                                                                                                                                                                                                                                                                                                                                                                                                                  68 IVGVELTHIPPKSIPKMAKKAKDLGAEIVVVH-GETVVEPVEEKTNYYASISEDVDILAH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 DETLXENNPTLLAVDRAPMTYSIDL-PGLASSDSFLQVEDPSNSSVRGAVNDLLAKWHQD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 THQGES-IENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVTATNDSRLYPGAL--LVV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 3.5%;
Local Similarity 18.8%;
                                                                                                                                                                                                    15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, J.A.; FitzGerald, L.M.; Clayton, R.A.; Gocayne, J.D.; Kerlavage, A.R.; Dougherty, B.A.; Tomb, J.F.; Adams, M.D.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Scott, J.L.; Geoghagen, N.S.M.; Weidman, J.F.; Fuhrmann, J.L.; Nguyen, D.; Utterback, T.R.; Kelley, J.M.; Peterson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C. Science (1996) 273:1058-1073

Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
                                    hypothetical protein 05050; hypothetical protein vor50-10 #formal_name Saccharomyces cerevisiae 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #54461 #type complete
hypothetical protein MJ1295 - Methanococcus jannaschii
#formal_name Methanococcus jannaschii
13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
10-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #length 218 #molecular-weight 24666 #checksum 9893
                                                                                                                 hypothetical protein YOR220w - yeast (Saccharomyces cerevisiae)
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                         05-Jun-
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translation not shown
S67113; S71722
                                                                                                                                                                       #type complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 2; Length 218;
Pred. No. 1.68e+00;
17; Mismatches 40; Indels
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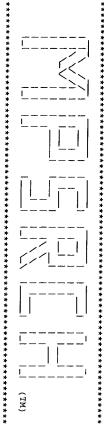
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Search completed: Fri
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                                                                                                                                                                                                                                                                          Query Match 3.3%;
Best Local Similarity 26.7%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #title Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of the yeast Saccharomyces cerevisiae. #cross-references MUID:96437977 #accession $71722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
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#map_position 15R
MARY #length 265 #molecular-weight 29255 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :CGSSICH CHARACTER DNA ##MOLECULE_TYPE DNA 1-265 ##label BOY 1-265 ##label BOY ##tesidues 1-265 ##label BOY ##cross-references EMBL:275128; NID:g1420509; PID:e252085; PID:g1420510; ##cross-references EMBL:275220w MIPS:YOR220w
                                                                                                                                                                                                                                                                                                                                                                                                                                ##cross-references EMBL:X92441; NID:g1050762; PID:g1050772
##note the nucleotide sequence was submitted to the EMBL Data
Library, October 1995
                                                                                                                                  143 SLNKGGSSLSPDKSSLESPTMLKLSTDSKPFSYQEPLPKLSRSSS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references EMBL:X92441; NID:g1050762; PID:g1050772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##status
                                                                                                                                                                               12 AMN-YDKKKLLTHQGESIENRFXKEGNQLPDE-FYVXE-RKKRSLSTNTSDIXVTATNDS
                                                                                            69
                                                                                                                                                                                                                          85 PMKLFVTESLLNNQ-HPR-SRSTDDAVSLQDNNLALLEDHRNKPLLSINTDPGVTGVDSS 142
                                                                                       RLY-PGALLVVDETLXENNPTL-LAVDRAPMTYSIDLPGLASSDS
48 secs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S60938

Galisson, F.; Dujon..B.

submitted to the EMBL Data Library, October 1995

Sequence and analysis of a 33 kb fragment from the right arm

of chromosome XV of the yeast Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galisson, F.; Dujon, B. Yeast (1996) 12:877-885
                       Sep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-265 ##label GAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence not shown; translation not shown
                       3 13:11:27 1999
                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                             Score 106; DB 2;
Pred. No. 2.17e+00;
                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                     Length 265;
                                                                                                                                                                                                                                                                          Indels 7;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                       7;
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Fri Sep 3 13:07:47 1999; MasPar time 14.50 Seconds 918.467 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-120-044-3-COPY (1-471) from devil20044.pep 3234

sequence: 1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 51.506; Variance 97.363; scale 0.529

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2221184 232100000000000000000000000000000000000	Result No.
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                                                MEDLINE; 87076517.

"CONC-TWASHITA Y., IWAMOTO M., MITSUI K., KA
"COLd-labile hemolysin produced by limited
from Clostriddium perfriggens.";
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from clostridium perfringens: significant homology with
streptolysin 0 and pneumolysin:
INFECT. IMMUN. 56:3235-3240(1988).
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"An upstream regulatory sequence stimulates expression perfringolysin O gene of Clostridium perfringens.";
INFECT. IMMUN. 59:137-142(1991).
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or send a
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MICROBIOL. IMMUNOL. 39:677-686(1995).
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EMBL; M36704; G144884; -.
EMBL; D49537; G1502275; -.
PIR; B43577; B43577.
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PROSITE; PS00481; THIOL_CYTOLYSINS;
PFAM; PFOLZ89; Thiol_cytolysin; 1.
TOXIN; HEMOLYSIS; CYTOLYSIS; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      model of its membrane form."; CELL 89:685-692(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). MEDLINE; 97325744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97113505.
FEIL S.C., ROSSJOHN J., ROHDE K., TWETEN R.K., F
"Crystallization and preliminary X-ray analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x-ray crystallography (2.4 angstroms). MEDLINE; 97113505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Role of the essential thiol group in from Clostridium perfringens."; EUR. J. BIOCHEM. 167:425-430(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NCTC 8237;
MEDLINE; 96123363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IWAMOTO M., OHNO-IWASHITA Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANCE OF THIOL-GROUP IN CHOLESTEROL
                     154 VSGAIDELVSKWNEKYSSTHTLPARTQYSESMYYSKSQISSALNVNAKVLENSLGVDFNA
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IDSVNDRTYPGALQLADKAFVENRPTILMVKRKPININIDLPGLKGENS-IKVDDPTYGK 153
                                                                                                                                                                                      NKAVNDFILAMNYDKKKLLTHQGESIENRFxKEGNQLPDEFVVxERKKRSLSTNTSDIxV
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Similarity 46.5%;
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K -> I (IN REF. 3).
RKP -> EA (IN REF. 2).
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X-ray analysis of a thiol-activated
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P13128; Q48747; Q57096; Q57206;
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
LISTERIOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
HLY OR LISA OR HLYA.
               the
                                                                                               STRAIN-F2365, F5782 (SEROTYPE 4B), AND F4233, F6789 (SEROTYPE 1/2B); VINES A., SWAMINATHAN B.; SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.
                                                                                                                                                                                                                                             RASMUSSEN O.F., BECK T., OLSEN J.E., DONS L., ROSSEN "Listeria monocytogenes isolates can be classified in types according to the sequence of the listeriolysin INFECT. IMMUN. 59:3945-3951(1991).
                                                                                                                                                                                                                                                                                                                                                                                           MENGAUD J. VICENTE M.-F., CHENEVERT J., PEREIRA J.M., GI
GICQUEL-SANZEY B., BAQUERO F., PEREZ-DIAZ J.-C., COSSART
"Expression in Escherichia coli and sequence analysis of
listeriolysin O determinant of Listeria monocytogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of the listeriolysin monocytogenes serotype 1/2a strain."; NUCLEIC ACIDS RES. 17:6406-6406(1989).
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
                                  between
                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
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European Bioinformatics Institute. The
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                                                                              SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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89366684.
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                         Institute of Bioinformatics
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PIR; A43505; A43505.
PROSITE; PS00481; THIOL_CYTOLYSINS;
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L; M24199; G149653; -.
L; W26035; G44112; -.
L; U25452; G887807; -.
L; U25443; G887016; -.
L; U25446; G887028; ALT_INIT.
L; U25449; G887864; ALT_INIT.
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                                                               IDHSGGYVAQFNISWDEVNYDPEGNEIVQHKNWSENNKSKLAHFTSSIYLPGNARNINVY
                                                                                                GKVDMVEDLIQEGSRFTADHPGLPISTTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
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                                                 LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
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Similarity 42.9%;
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M -> I (IN STRAIN F2365).

V -> I (IN STRAINS F2365, F F6789 AND 12067).

K -> S (IN STRAINS F2365, F F6789 AND 12067).
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  (See http://www.isb-sib.ch/announce/
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92182018.
HAAS A., DUMBSKY M., KREFT J.;
"Listeriolysin genes: complete sequence of ilo from Listeria ivanovii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILO.
LISTERIA IVANOVII.
BACTERIA; FIRMICUTES;
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PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
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                                                                                    LDHSGAYVARFNVTWDEVSYDANGNEVVEHKKWSENDKDKLAHFTTSIYLPGNARNINIH
                                                                                                                   GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                                     GDLSKLRDILKQGANFDKKNPGVPIAYTTNFLKDNQLAVVKNNSEYIETTSKAYSDGKIN 419
                                                                                                                                                                                                                                         SGEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGR
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                            AKECTGLAWEWWRTVVDDRNLPLVKNRNVCIWGTTLYPAYSDTVDN 525
                                                                                                                                                                               QVYLKLETTSxSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                                                                                           DIFVKLSTSSHSTRVKAAFDTAFKGKSVKGDTELENIIQNASFKAVIYGGSAKDEVEIID 359
                                                                                                                                                                                                                                                                                                   AVNDLLAKWHQDYGQVN-NVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
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                                                         LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1524; DB 1;
Pred. No. 1.26e-296;
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BINDING TO CHOLESTEROL (BY SIMILARITY).
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P31830;
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01-JUL-1993 (REL. 2
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SEQUENCE
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ACT_S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Listeriolysin Genes: complete sequence of ilo from Listeria ivanovii and of iso from Listeria seeligeri.";
BIOCHIM. BIOPHYS. ACTA 1130:81-84(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTIC CELL MEMBRANES.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                   GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                                                                                                                              QVYVKLSSSSHSNKVKTAFEAAMSGKSVKGDVELTNIIKNSSFKAVIYGGSAKEEVEIID
IDHSGGYVAQFNISWDEVSYDENGNEIKVHKKWGENYKSKLAHFTSSIYLPGNARNINIY 481
                                                                                                                                                                                                                                                                                                                                                  DGKYQEEYISFKQIYYNINYNEPTSPSKFFGGSYTKEQLDALGVNAENPPAYISSYAYGR
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                                                                                                                GNLGELRDILKKGSTYDRENPGVPISYTTNFLKDNDLAVVKNNSEYIETTSKSYTDGKIN
                                                                                                                                                                          QVYLKLETTSxSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                                                                                                                                                                           SGEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGR
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Similarity 42.5%;
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26, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
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59181 MW;
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Pred. No. 3.48e-286;
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BINDING TO CHOLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALOUF J.E., GEOFFROY C., GILLES A.M., FALMAGNE (IN) RAPPUOLI R., ALOUF J.E., FALMAGNE P. (EDS: BACTERIAL PROTEIN TOXINS, PP.49-50, GUSTAV FISH STUTTGART (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (REL.
01-NOV-1991 (REL.
15-DEC-1998 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEOFFROY C., MENGAUD J., ALOUF J.E., COSSART P.;
"Alveolysin, the thiol-activated toxin of Bacillus alvei, is
homologous to listeriolysin O, perfringolysin O, pneumolysin,
streptolysin O and contains a single cysteine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACY_PAEAL P23564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 33-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIA; FIRMICUTES; PAENIBACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAENIBACILLUS ALVEI (BACILLUS ALVEI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALVEOLYSIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00481; THIOL_CYTOLYSINS PFAM; PF01289; Thiol_cytolysin; 1. HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M62709; G142473; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 ARECTGLFWEWWRTVIDDRNLPLVKNRNVSIWGTTLYPRHSNNVDN 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COXIN;
104
                                                                                   70
                                                                                                                                                                                                10
                                                                                                                                                                                                                                                   44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIOL. 172:7301-7305(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAGLNYNRNEVLAIQGDQISSFVPKEGIQSNGKFIVVERDKKSLTTSPVDISIVDSITNR 103
                                                                                                                                      TYPGAIQLANKDFADNQPSLVMAARKPLDISIDLPGLKNENT-ISVQNPNYGTVSSAIDQ 162
                                                                                                                                                                                       ILAMNYDKKKLLTHQGESIENRFxKEGNQLPDEFVVxERKKRSLSTNTSDIxVTATNDSR 69
                                                                                   LYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRGAVND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEMOLYSIS;
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                    501 AA;
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                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20, CREATED)
20, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOLYSIS; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIOL_CYTOLYSINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     501
                                                                                                                                                                                                                                                                                                                                 45.2%;
41.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 55268 MW;
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                                                                                                                                                                                                                                                                                                       121; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                          Score 1461;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALVEOLYSIN.
BINDING TO CHOLESTEROL (BY SIMILARITY)
A -> L (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                 8DF2C94A CRC32;
                                                                                                                                                                                                                                                                                                                                 No. 1.24e-282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           501
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                                                                                                                                                                                                                                                                                                                                                             Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACILLACEAE;
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Matches
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Best Local
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G streptococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKUMURA K., HARA A., TANAKA T., NICHIGUCHI I., MINAMIDE W.,
IGARASHI H., YUTSUDO T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREPTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA;
                                                                                                                                                                                                                                         PFAM; PF01289; Thiol_cytolysin; 1.
HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and sequencing the streptolysin O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95102113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430
                                                                                                                                                                                                                                                                                           PROSITE; PS00481; THIOL_CYTOLYSINS;
                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 LLAKWHQDYGQVNNVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHSGEKQ 189
                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTIC CELL MEMBRANES.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LETTSKSNDVQTAFKLLLNNPSIQASGQYKDIYENSSFTAVVLGGDAQTHNQVVTKDFNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLAWEWWRTVVDEYNVPLASDINVSIWGTTLYP 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKIRECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYVAQFEVYWDEFSYDADGQEIVTRKSWDGNWRDRSAHFSTEIPLPPNAKNIRIFARECT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQVYLK
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                                                                                                                                                                                                                                                                                                                      D16824; G498301;
190;
                                                                                                                                                                                                       HEMOLYSIS; CYTOLYSIS;
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIRMICUTES;
                                                                                                   37
533
574 AA;
Conservative
                        43.6%;
41.6%;
                                                                                                         63991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
  106;
                              Score 1409; DB 1;
Pred. No. 4.24e-271;
                                                                                                                            BY SIMILARITY.
STREPTOLYSIN O.
BINDING TO CHOLESTEROL
                                                                                                                                                                                                             SIGNAL
                                                                                                         9BBF31B4 CRC32;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462
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                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes of group C
  160;
                                               Length 574;
  Indels
                                                                                                                                  (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
  1;
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  Gaps
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                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   PROSITE; PS00481; THIOL_CYTOLYSINS; PFAM; PF01289; Thiol_cytolysin; 1. HSSP; P19995; 1PFO.
                                                                                                    EMBL; M18638; G153811; -. PIR; A43507; A43507.
                                                                                                                                                                                                                                                                                                                                                                                                               KEHOE M.A., MILLER L., WALKER J.A., BOULNOIS G.J.;
"Nucleotide sequence of the streptolysin O (SLO) gene:
ioumologies between SLO and other membrane-damaging, thi
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01-FEB-1991 (REL.
15-JUL-1998 (REL.
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                                                                                                                                                                                                                                                                                          EUKARYOTIC CELL MEMBRANES.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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                                    HEMOLYSIS;
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                               CYTOLYSIS; SIGNAL; PLASMID
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17, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)
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STREPTOLYSIN O.
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15-JUL-1998 (REL. 3
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       G streptococci.;
DNA SEQ. 4:325-328(1994).
                                                                                                                                               -!- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                               OKUMURA K., HARA A., TAN IGARASHI H., YUTSUDO T.;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                            "Cloning and sequencing the streptolysin O genes of group C and
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                                                                                                                                                                      FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTALNING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.
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Similarity 41.8%;
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571 AA;
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36, LAST ANNOTATION UPDATE
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63638 MW;
                                                                                                                                                                                                                                                                                                              TANAKA T., NICHIGUCHI I., MINAMIDE W.
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Pred. No. 7.07e-271;
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Best Local S
Matches 18
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15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
15-JUL-1998 (REL. 3
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PROSITE; PS00481; THIOL_CYTOLYSINS;
PROSITE: PS00481; THIOL_CYTOLYSIN; 1.
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the Euro
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                                                                                                                          SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS:
-i- FUNCTION: SULFHYDYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL-
CONTALNING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.
CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-RIMD 206001;
                                                                                                                                                                                                                                                                                       BACILLUS CEREUS
                                                                                                                                                                                                                                                                                                       HEMOLYSIN PRECURSOR
                                                                                                                                                                                                                                                                        BACTERIA; FIRMICUTES;
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                                                                            EUKARYOTIC CELL MEMBRANES (BY SIMILARITY).
FUNCTION: HEMOLYTIC ACTIVITY AGAINST RED BLOOD CELL.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTDRTYPAALQLANKGFTENKPDAVVTKRNPQKIHIDLPGMGDKAT-VEVNDPTYANVST 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQ
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                     BACCE
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                                                                                                                                                                                                                                                                                                                     (REL. 36, CREATED)
(REL. 36, LAST SEQUENCE UI)
(REL. 36, LAST ANNOTATION
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Pred. No. 2.48e-267;
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STREPTOLYSIN O.
BINDING TO CHOLESTEROL (BY SIMILARITY).
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HSSP; P19995; 1PFO.
                     BEQUENCE AND SECULARIES AND Y.P.P., WEYLER W., CHEN S., SALACH POWELL J.F., HSU Y.P.P., WEYLER W., CHEN S., SALACH ANDRIKOPOULOS K., MALLET J., BREAKEFIELD X.O.;
"The primary structure of bovine monoamine oxidase and sequences of bovine monoamine oxidase
                                                                                                                                                                                                                                                                                                                                                    01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATAMINE OXIDASE [FLAVIN-CONTAINING] A (EC 1.4
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                                                                                                                                                                                                                             BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDI
ARTIODACTYLA; RUMINANTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 P21398;
01-MAY-1991
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flavoenzymes.";
BIOCHEM. J. 259:407-413(1989)
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Similarity 39.58;
                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                             (BOVINE).
METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; E
METAZOA; CHORDATA; BOVOIDEA; BOVIDAE;
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>485 HEMOLYSIN.
466 BINDING TO CHOLES
485
485
45 45208ABA CRC32;
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                                                    type
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                                                                                                                                                                                                                                                                EUTHERIA;
                                                                                                                                                                                                                                   BOVINAE;
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Best Local
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P10507;
                                                                                                                                                                                                                                                                                                                               (EC 3.4.24.64) (BETA MPP) (PEP).

MAS1 OR MIF1 OR YLR163C OR L9632.10.

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1989 (REL. 11, CREATED)
01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT
                                  STRAIN=S288C
                                                                                                                                             "MASI, a gene
subunit of the
                                                                                                                                                                                              MEDLINE; 88312592.
WITTE C., JENSEN R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                               SEQUENCE FROM N.A
                                                                                                                EMBO J. 7:1439-1447(1988).
                                                                                                                                                                                                                                                                                                        SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X15609; G524; EMBL; X15609; G525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEUROTRANSMITTER DEGRADATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OXIDOREDUCTASE; FLAVOPROTEIN; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 GAYVAQYYITWNELSYDHQGKEVLTPKAWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 LETTSxSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVTGKVDM 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MESLQKTSDAGQMFDVVVIGGGISGLSAAK-LLAEHEVNVLVLEARERVGGRTYTVRNEH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    II(2)0(2).
COFACTOR: FAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: CATALYZES THE OXIDATIVE DEAMINATION OF BIOGENIC AND XENOBIOTIC AMINES AND HAS IMPORTANT FUNCTIONS IN THE METABOLISM NEUROACTIVE AND VASOACTIVE AMINES IN THE CENTRAL NERVOUS SYSTEM AND PERIPHERAL TISSUES. MAO-A PREFERENTIALLY OXIDIZES BIOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAYL-DYNNLWRTM--DNMGKEIPADAPWE
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Similarity 19.3%;
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                                                                                                                                          the mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406
     ANDREWS
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                               AB972;
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     ŝ
                                                                                                                              YAFFE M.P., SCHATZ G.;

1 for yeast mitochondrial assembly,
ndrial processing protease.";
BRINKMAN R., COOPER J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 117; DB 1;
Pred. No. 2.05e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398
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                                                                                                                                                                                                                                                                                                                                  SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECURSOR
  DING
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DU Z.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
NOP5_YEAST
Q12499;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use as long as 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00143; INSULINASE; 1. PFAM; PF00675; Insulinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purified precursor protein.";

J. BIOL. CHEM. 266.6416-6423(1991).

J. BIOL. CHEM. 266.6416-6423(1991).

PUNCTION: THE MITOCHONDRIA PROCESSING PROTEASE CLEAVES PRESEQUENCES FROM MITOCHONDRIAL PROTEIN PRECURSORS.

-!- CATALYTIC ACTIVITY: RELEASE OF N-TERMINAL TRANSIT PEPTIL PRECURSOR PROTEINS IMPORTED INTO THE MITOCHONDRION, TYPIARG IN POSITION P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M.,
JOHNSON D., JOHNSTON L., LANGSTON Y., LATREILLE P., LE T.,
MARDIS E., MENEZES S., MILLER N., NHAN M., PAULEY A., PELUSC
RIFKEN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D.,
WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.,
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROLASE; METALLOPROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X07649; G3887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- COFACTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY
-1- SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.
-1- SUBCELULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                   268
                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                                                                                                  125
                                                                                                                                                                                                                                                                                                                                                                      154 TAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHSGEKQIQIVNxKQIYYTVSV-DAVKNPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YANG M., GELI V., OPPLIGER W., SUDA K., JAMES P., SCHATZ G. "The MAS-encoded processing protease of yeast mitochondria. Interaction of the purified enzyme with signal peptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                     ILSDILTKSVLDNSAIERERDVIIRESEEVDKMYDEVVFDHLHEITYKDQPLGRTILGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; U51921; G1234852;
S00552; S00552.
A38734; A38734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSULINASE FAMILY.
                                                                                                                                                                              KGVKVAPQTEWKQ-ILDNTEVKAVILGG
                                                                                                                                                                                                                               KNIKSITRTDLKDYITKNYKGDRMVLAG
                                                                                                                                                                                                                                                                           VFQDTVTVEDLKQRGISAERPLVYI-Sx-VA--YGRQVYLKL-ETTSxSxEVEAAFEALI
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91177897.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 1;
Pred. No. 4.15e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BETA SUBUNIT.
ZINC (BY SIMILARITY)
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 462;
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STANDARD

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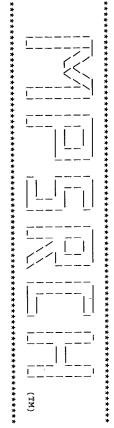
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288C / FY1679;
PEARSON B.M., HERNANDO Y., WOLF S.S., KALOGEROPOULOS SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOLAR PROTEIN NOP5.
NOP5 OR YOR310C OR O6108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTA; FUNGI; AS SACCHAROMYCETACEAE;
STRAIN-PV/2,
STRAIN-PV/2,
MEDLINE; 94320770.
WHEN B., SLEYTR U.B., LUBI'
                                                                                                                                                                                                                                                                             01-JUN-1994 (REL. 29, CREATED)
01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
S-LAYER PROTEIN PRECURSOR (SURFACE LAYER PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF056070; G3170533; -. SGD; L0004000; NOP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-W30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (REL. 37,
                                                                         STRAIN-PV72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEAR PROTEIN; RRNA PROCESSING DOMAIN 441 511 ASP,
                                                                                                                                                                                                                            BACILLUS
                                                                                                                                                                                                                                                                                                                                                                                     SLAP_BACST P35825;
                                                                                                                                                                                                    BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOL. CHEM. 273:16453-16463(1998).
FUNCTION: REQUIRED FOR PRE-18S RRNA PROCESSING SUBCELLULAR LOCATION: NUCLEAR; NUCLECLUS.
SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8S rRNA processing in yeast.";
OL. CHEM. 273:16453-16463(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGDLL-LDHSGAYVAQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSLISLAKSPASTIQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X90565; G940841; -.
Z75217; E252143; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                                                                                                                                                                                                                               STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNGI; ASCOMYCOTA; HEMI
CETACEAE; SACCHAROMYCES:
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llarity 22.1%;
Conservative
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56956 MW;
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                                                                                                                                                                                                    BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                           LUBITZ W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WOLF S.S., KALOGEROPOULOS A.,
                sbsA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108; DB 1; Le
Pred. No. 3.10e-01;
39; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                   encoding the 130-kDa
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component required
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 surface-layer protein of Bacillus stearothermophilus strain PV72. "; GENE 145:115-120(1994).
                                                                                                                                                                "The nucleotide sequence of the H-1r gene of Salmonella rubislaw.";
NUCLEIC ACIDS RES. 14:8227-8227(1986).
-!- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
-!- INDIVIDUAL SALMONELLA SEROTYPES USUALLY ALTERNATE BETWEEN THE PRODUCTION OF 2 ANTIGENIC FORMS OF FLAGELLA, TERMED PHASE-1 AND PHASE-2, EACH SPECIFIED BY SEPARATE STRUCTURAL GENES.
-!- SIMILARITY: TO OTHER BACTERIAL FLAGELLINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIA IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
FLAGELLIN (PHASE-1-R FLAGELLIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLIC_SALRU
P06175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S34365; S34365.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLIC OR FLAF OR HAG.
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                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 10717;
MEDLINE; 87040788.
                                                                                                                                                                                                                                                                                                                                                                                                                          SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-RFTADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAALTPKVESVS-AINTQNKAVELTAVPVNGT-LKLQLSAAANEDTVNVNTVRIYKVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                             JOYS T.M.;
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Pred. No. 4.15e-01;
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Search completed: Fri Sep 3 13:08:42 1999 Job time : 55 secs.
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                                                                                                                                                                                                                                                                                                                                                         EMBL; X04505; G47471; -.
PIR; S07375; S07375.
PFAM; PF00669; Flagellin_N; 1.
PFAM; PF00700; Flagellin_C; 1.
FLAGELLA.
INIT_MET 0 0
SEQUENCE 492 AA; 51285 MW; E
                                                                                                                                                                       291 ILGGDPSSGARVVTGKVDMVEDLIQEGSRFTA 322
                                                                       263 T-AGFPSTATKDVKQTQQENADLTEAKAALTA 293
                                                                                                           232 RPLVYISXVAYGRQVYLKLETTSXSXEVEAAFEALIKGV-KVAPQTEWKQILDNTEVKAV 290
                                                                                                                                                                                                                               113 LQVEDPSNSSVRGAVNDLLAKWHQDYGQVNNVPARXQYEKITAHSMEQ-LKVKFGSDFEK 171
                                                                                                                             207 TTLGGTPAIT-G-D--LKFDDTTGKYYADVSGTTAKDGYYEVTVAADGKYTLTGTPTGPI 262
                                                                                                                                                                                                                                                  0 0
492 AA; 51285 MW; E0DB5DB4 CRC32;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Fri Sep 3 13:08:59 1999; MasPar time 29.05 Seconds 884.788 Million cell updates/sec

Tabular output not generated.

Run on:

Description: Perfect Score: Title:

Sequence: >US-09-120-044-3-COPY (1-471) from dev1120044.pep 3234 1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Scarched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

isp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Statistics: Mean 49.380; Variance 93.518; scale 0.528

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

20 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
1775 1370 1302 124 118 1113 1113 1113 1112 107 107 106 106 106 107 107 107 107 107 107 107 107 107 107	Score
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0.00e+00 0.00e+00 3.48e-248 1.83e-03 1.29e-02 6.29e-02 3.58e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01 5.33e-01	Pred. No.

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SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF043556; G3309561; -.
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                                                                                                                                                                                                                                                   Q48772 PRELIMINARY;
Q48772;
01-NOV-1996 (TREMBLREL, 0
01-NOV-1996 (TREMBLREL, 0
01-NOV-1998 (TREMBLREL, 0
                     SEQUENCE FROM N.A. STRAIN=11984, TYPE 1; MEDLINE; 96118685.
                                                                                                                                                       LISTERIA MONOCYTOGENES BACTERIA; FIRMICUTES; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     novel member of the thiol-activated cytolysin family.",
J. BACTERIOL. 179:6100-6106(1997).
EMBL; U84782; G2252800;
PFAM; PF01289; Thiol_cytolysin; 1.
SEQUENCE 534 AA; 57873 MW; B0C14CA8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998
01-JAN-1998
01-NOV-1998
RASMUSSEN O.F.,
                                                                                                                              LISTERIA
                                                                                                                                                                                                                                LISTERIOLYSIN O (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARCANOBACTERIUM PYOGENES.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BBR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTINOMYCETALES; ACTINOMYCINEAE; ACTINOMYCETACEAE; ARCANOBACTERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          418 VRNLSVKIRECTGLAWE-WWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 ARNIHVEAGEATGLAWDFWW-TVINKKNLPLVPHREIVLKGTTLNPWVEDNV 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLINGTON S.J., JOST B.H., CUEVAS W.A., BRIGHT K.R., SONGER J. TiThe Arcanobacterium (Actinomyces) pyogenes hemolysin, pyolysin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BILLINGTON S.J., JOST B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 97464437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYOLYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 VTATNDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ETGVDKYIRGLKYDPSGVLAVKGESIENVPYTK-DQLKDGTYTVFKHERKSFNNLRSDIS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YKSGEITFRHGGGYVAKFRLKWDEISYDPQGKEIRTPKTWSGNWAARTLGFRETIOLPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGVEVATGNIDALKKIIKEESTYSTKVPAVPVSYAVNFLKDNQLAAVRSSGDYIETTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGRQVYLKLETTSXSXEVEAAFEALIKG--VKVAPQ--TEWKQILDNTEVKAVILGGDPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AIHKRERQVAIASFKQIYYTASVDTPTSPHSVFGPNVTAQDLKDRGVNNKNPLGYISSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVTQGLNGLLDGWIQRNSKYPDHAAKISYDETMVTSKRQLEAKLGLGFEKVSAKLNVDFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFDANNAHVYPGALVLANKDLAKGSPTSIGIARAPQTVSVDLPGLVDGKNKVVINNPTKS
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Similarity 40.0%;
                                                                                                                                                    FIRMICUTES;
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GIREMBLREL.
GIREMBLREL.
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                                                                                                                                               BACILLUS/CLOSTRIDIUM
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05, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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LAST SEQUENCE ANNOTED
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Pred. No. 3.48e-248;
                                                                                                                                                                                                                                                   SEQUENCE UPDATE)
ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                 GROUP;
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SKOUBOE

P.,

DONS

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ROSSEN L.,

OLSEN J.E.;

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Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                          RASMUSSEN O.F., SKOUBOE P., DONS L., ROSSEN L., OLSEN J.E.;
"Listeria monocytogenes exists in at least three evolutionary
evidence from flagellin, invasive associated protein and
listeriolysin O genes.";
MICROBIOLOGY 141:2053-2061(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q48773 PRELIMINARY;
Q48773;
Q1-NOV-1996 (TREMBLREL 01,
Q1-NOV-1996 (TREMBLREL 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        evidence from flagellin, invasive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 listeriolysin O genes.";
MICROBIOLOGY 141:2053-2061(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Listeria monocytogenes exists in at least three evolutionary lines:
                                                                                                                                               O68518 PRELIMINARY; PRT; 450 AA.
O68518; O1-AUG-1998 (TREMBLREL 07, CREATED)
O1-AUG-1998 (TREMBLEEL 07, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLEEL 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 49.7 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LISTERIA MONOCYTOGENES. BACTERIA; FIRMICUTES; I
                   MEDLINE: 96347136.
TRUDEAU K.G., WARD M.J., ZUSMAN D.R.;
"Identification and characterization regulator necessary for swarming and myxococcus xanthus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=206.1.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                                                                                             BACTERIA; PROTEOBACTERIA; DELTA MYXOCOCCCALES; CYSTOBACTERINEAE;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                               STRAIN-DZF1
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                       MYXOCOCCUS XANTHUS
                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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                                                                                                                                                                                                                                                         284
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                                                                                                                                                                                                                                                         NTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYT
                                                                                                                                                                                                                                                                               NSSFKAVIYGGFAKDEVQIIDGNLGDLRDILKKGATFNRETPGVPIAYT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X85855; G940601;
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                                                                                                                                                                                                                                                                                                      3.6%;
larity 34.7%;
Conservative
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50
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            20:645-655(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5368 MW;
                                                                                                                                                                                                                                                                                                                                                      5429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 124; DB 2;
Pred. No. 1.83e-03;
14; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAST SEQUENCE UP
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                                                                                                                                                                                                                                                                                                      Pred.
14; N
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                                                                                                                                                                                                                                                                                                                                                      A4B59721 CRC32;
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                                                                                                                SUBDIVISION; MYXOBACTERIA; MYXOCOCCUS:
                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                  No. 1.29e-02
                                 of FrzZ, a novel response fruiting-body formation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                             DB 2;
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RESULT 7
ID Q12098
AC Q12098;
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Best Local
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Best Local Similarity
            Query Match
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SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF049107; G2947295; -.
HYPOTHETICAL PROTEIN.

ACCOC MD. STAKFOG7 CRC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=DZF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
CHROMOSOME XII READING FRAME ORF YLR135W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L9606.6 OR L3140.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                                                        WATERSTON
SUBMITTED
                                                                                                                                                                                                                                             JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., D
FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KU
HALLSWORTH K., HAWKINS J., HILLIER L., JERR M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., M
MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES
TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DELIUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA;
                                   EMBL; Z73307; E245572; -
EMBL; U53881; G1256901;
EMBL; X91258; G995701; -
SEQUENCE 748 AA; 8436
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (MAY-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      WILSON R.,
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233
                                                                                      SUBMITTED (SEP-1995)
                                                                                                                 STRAIN-S288C;
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                               STRAIN=S288C (AB972);
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                        SUBMITTED (APR-1996)
                                                                                                     ELIUS H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 HLPGRLPVGLHPETGELELVREMKVGGKTFVPNAVGALLPPGYTRTFLPGEV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLVLVTSDMTFAPKL-LFADPKGRVMEHPYLLATLRSGEELVPPQD-KPIPLPSTG-RLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLVYI-SxVAYGRQVYLKLETTSxSxEVEAAFEALIKGVKVAPQTEWKQI-LDNTEVKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILGGDPSSGARVVTGKVDMVEDLIQEGSRFTADHPG--LPISYTTSFLRDNV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 30; Conser
                                                                                                                                                      (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                    (APR-1996) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                      WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEBLING U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49686 MW;
3.5%;
18.8%;
                                       84361
                                                                                       TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                        TO
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                        TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                        EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                    EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                        EMBL/GENBANK/DDBJ
                                       WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 6.29e-
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113; DB 2;
Pred. No. 6.29e-02;
Score 112; DB 3;
Pred. No. 8.58e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E3A6FC67 CRC32;
                                       4900A1F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             748
                                         CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                         DATA BANKS
                                                                                                                                                         DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SACCHAROMYCETALES;
            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                           H., DU J., KUCABA T.,
                                                                                                                                                                                                                                         ., VAUDIN M.,
                                                                                                                                                                                                                                                                            MENEZES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                       01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
CHROMOSOME XV READING FRAME ORE YOR220W.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

KURLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., WERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

SCOTT J.L., GEOGHAGEN N.S.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOBSE C.R., VENTER J.C.;
THIERRY A.,
                                SEQUENCE FROM N.A.
                                                                  SACCHAROMYCETACEAE;
                                                                                                                                                                                                         Q12044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67570; G1591933; -. HYPOTHETICAL PROTEIN. SEQUENCE 218 AA; 24666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q58691;
Q58691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
SCIENCE 273:1058-1073(1996).
-!- SIMILARITY: STRONG, TO A.FULGIDUS AF1550 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHANOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHANOCOCCUS JANNASCHII.
ARCHAEA; EURYARCHAEOTA; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                   153 ITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHSGEKQIQIVNxKQIYYTVSVDAVKNPGD 212
                                                                                                                                                                                                                                                                      213 V-FQDTVTVEDLKQRGISAE 231
                                                                                                                                                                                                                                                                                                        127 PGFIDKETAENLKENDIFVE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 YGQVNN-VPARXQY-EKI-T-AH-SMEQLKVK-FGSD-FEKTGNSLDI-DFNSVHS 185
                                                                                                                                                                                                                                                                                                                                                                   68 IVGVELTHIPPKSIPKMAKKAKDLGAEIVVVH-GETVVEPVEEKTNYYASISEDVDILAH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. THERMOAUTOTROPHICUM MTH576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDHLTELIEAFPDFLERIYTFEPIPLNELIEKLFSAEPFVSQIDEMTIREWADVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DETLXENNPTLLAVDRAPMTYSIDL-PGLASSDSFLQVEDPSNSSVRGAVNDLLAKWHQD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOSMKELROSLKTVGLKPMRTKVELIOSLQTASQILSTANPDNKGEHGGVANF-SK-IEI 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THOGES-IENRFXKEGNOLPDEFVVXERKKRSLSTNTSDIXVTATNDSRLYPGAL--LVV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEEEETEFDDQFCIADIQLVDSSKISTKDSTQNPTTSNDIIDTSAASSIASPEKFCEIMM 626
                                                                                                                                                                                                                                                                                                                                                                                                          h 3.3%;
Similarity 26.3%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
              FAIRHEAD C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
 DUJON
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24666 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REL. 06,
REL. 06,
REL. 06,
MJ1295.
              GAILLON L.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 1;
Pred. No. 3.95e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST ANNOTATION UPDATE)
                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFC99AB9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE UPDATE)
            GALISSON F.,
                                                                                                                                                                                                  265 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ã
                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 218;
        MICHAUX G.,
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                       2;
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Qy

Qy

309 MVEDL-IQEGSRFTADHPGL 327

QΥ Вþ

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                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                         KIENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRPIDES N.C., FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU OVERBEEK R., GOCAYNE J.D., WEIDMAN J.F., MCONALD L., UTTERBACK T. COTTON M.D., SPIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                               HYPOTHETICAL PROTEIN. SEQUENCE 501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 10
028947 PRELIMINARY;
028947;
01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALISSON F., DUJON B.;
SUBMITTED (007-1995) TO EMBL/G:
EMBL; 275128; E252085; -.
EMBL; X92441; G1050772; -.
SEQUENCE 265 AA; 29255 MW;
                                                                                                                                                                              TIGR;
                                                                                                                                                                                          EMBL; AE001012; G2649254; -.
                                                                                                                                                                                                          sulphate-reducing archaeon Archaeoglobus NATURE 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 98049343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TREMBLREL. 01-AUG-1998 (TREMBLREL.
                                                    217 LVAVNDSGVVEGRIVE-VNGVKVSSVDDVKAVLQNAEIAEIKIVNGDEIRILSVPAVMGV 275
                                                                                                                                                                                                                                  "The complete genome sequence of the hyperthermophilic,
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARCHAEOGLOBUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARCHAEOGLOBUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONSERVED HYPOTHETICAL
276 KVIGLYTENGEKFPAELAGI 295
                                                                                                                                                                                                                                                      ZENTER J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (JUL-1996) TO [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                    y Match
3.3%;
Local Similarity 27.5%;
hes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 SLNKGGSSLSPDKSSLESPTMLKLSTDSKPFSYQEPLPKLSRSSS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 RLY-PGALLVVDETLXENNPTL-LAVDRAPMTYSIDLPGLASSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 PMKLFVTESILNNO-HPR-SRSTDDAVSLQDNNLALLEDHRNKPLLSINTDPGVTGVDSS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 3.3%;
Local Similarity 26.7%;
                           LETTSxSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAV-ILGGDPSSGARVVTGKVD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMN-YDKKKLLTHQGESIENRFXKEGNQLPDE-FVVXE-RKKRSLSTNTSDIXVTATNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                              55698 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARCHAEOGLOBALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05,
07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GENBANK/DDBJ DATA BANKS
                                                                                    Score 107; DB 1;
Pred. No. 3.95e-01;
24; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 106; DB 3;
Pred. No. 5.33e-01;
26; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                            5EE0081E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2D5DD78E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE UPDATE:
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Best Local
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Best Local
                                                                                                              EMBL; ALVEL
HYPOTHETICAL PROTEL
TOTAL 814 AA;
                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
BEVAN M., VAN DER SCHUEREN J., CHUANG Y-J., VOET M.,
VOLCKAERT G., BANCROFT I., MEWES H.W., MAYER K.F.X.,
CHRMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK E.C., SENSEN C.W., GAASTERLAND T., SAFFER J.D., FREDRICKSON J.K.; "Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromaticivorans strain F199."; SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AF079317; G3378338; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 11
085906
                                                                                                                                                                                                                                                                                                                                                                                           LT 12
065715
                                                                                                                                          SEQUENCE FROM N.A.
EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITTED (APR-1998) TO EMBL/GENBA
EMBL; AL022580; E1287635; -.
                                                                                                                                                                                                                                                                           ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSI
                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TREMBLREL 07, CREATED)
01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL 07, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLASMID PNLI
BACTERIA; PR
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                                                                                                                                                                                                                                                                     CAPPARALES;
                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL 91.9 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                               065715;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 NHHNDAVLECYAAWYGANYGRR-RQSQT-RQWIRGGKIVTSEFRSPEVQLEGDIHRFAII 196
 788
                         187
                                          729 EMHSKNVHPNKITYTYMIGGYARDGNVTEASRLLNEMREKGIVPD-SITYKEFIYGYLKQ 787
                                                                                                                                                                                                                                                                                                                                                                                                                                        425 IR
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GGV-LEAFKGSDE-EN-YAAIIEG
                      EKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXV-AYGRQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                          426
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                                                                      Similarity 21; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     710 AA;
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(TREMBLREL.)
(TREMBLREL.)
PROTEIN B.
                                                                                                                                                                                                                                                                  BRASSICACEAE; ARABIDOPSIS
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                 PROTEIN
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                                                                                 3.3%;
                                                                                                                    91943 MW;
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bred. No. 3.95e-01;
                                                                   Score 106; DB 10;
Pred. No. 5.33e-01;
27; Mismatches 31
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LAST SEQUENCE UP
LAST ANNOTATION
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                                                                                                                    A41B8987 CRC32;
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SCHUELLER
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087083;
01-NOV-1998
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       030524;
01-JAN-1998
01-JAN-1998
01-NOV-1998
                                                                    WANG B., KRAIG E., KOLODRUBETZ D.;
"A new member of the S-layer protein family: characterization crs gene from Campylobacter rectus.",
INFECT. IMMUN. 66:1521-1526(1998).
EMBL; AFO10143; G2459961;
EMBL; AFO10143; G2459961;
SEQUENCE 1361 AA; 144385 MW; CAFE081F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     determination and function of the recomb FEMS MICROBIOL. LETT. 166:275-281(1998). EMBL; AB001876; D1034498; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAMPYLOBACTER RECTUS.
BACTERIA; PROTEOBACTERIA;
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                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                                           STRAIN=314
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                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Local Similarity nes 38; Consen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VILGGD
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Similarity 20.4%;
38; Conservation
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(TREMBLREL.
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  Conservative
                    3.3%;
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Score 106;
Pred. No. 5.
49; Mismatc
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Pred. No. 5.33e-01;
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  Mismatches
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  .33e-01;
ches 89;
                                           DB 2;
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                                         Length 1361;
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Indels
10;
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RESULT AC OSC SERVING SOLUTION OF THE HEILER ACCORDANCE 
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Search completed: Fri Sep
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C 063460;

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)

DT 01-NOV-1998 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

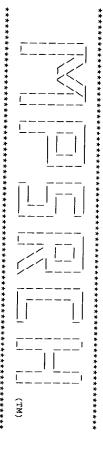
"POT.INE-RICH PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ.
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Best Local Similarity 20.4%;
Matches 38; Conservative
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MEDILINE: 89066721.

HEMSCHOOTE K., PEETERS B., DIRCKX L., CLAESSENS F., DE CLERCQ N.,
HEYNS W., WINDERICKX J., BANNWARTH W., ROMBAUTS W.;

"A single 12.5-kilobase androgen regulated mRNA encoding multiple
proline-rich polypeptides in the ventral prostate of the rat.";

J. BIOL. CHEM. 263:19159-19165(1988).
                                                                                                                                                                                                                                                                                                                              3570
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J. BIOL. CHEM. 0:0-0(0).
EMBL; M86514; G206409; -
NON_TER 1
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
CCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
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                                 3 13:10:22 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 11; Length 5027; Pred. No. 3.95e-01; 50; Mismatches 87; Indels 11
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Aug 30 16:14:04 1999; MasPar time 18.38 Seconds 544.892 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score:

>US-09-120-044-4
(1-471) from US09120044.pep
3127
1 MANKAVNDFILAMNYDXXKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part20 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39

Statistics: Mean 35.164; Variance 168.905; scale 0.208

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Qy 121 SSVRGAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDF 180
	Db 121 ssvrgavndllakwhqdygqvnnvparmqyekitahsmeqlkvkfgsdfektgnsldidf 180
	Qy 61 XVXATXDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSN 120
	Db 61 svtatndsrlypgallvvdetllennptllavdrapmtysidlpglassdsflqvedpsn 120
	Qy 1 MANKAVNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDI 60
	Db 1 mankavndfilamnydkkkllthqgesienrfikegnqlpdefvvierkkrslstntsdi 60
0	
	Query Match 100.0%; Score 3127; DB 1; Length 471; Best Local Similarity 04.5%. Bood No. 1 100.050
	Sequence 471 AA;
	CC making them useful in vaccination against pneumonia and associated CC meningitis, bacteriaemia etc
	PS Claim 5: Page 11: 25mp: English
	protective vaccines against Strept
	PI WALKER JA;
	(PATO/) PATON J C.
	16-DEC-1988;
	PF 15-DEC-1989; AU0539.
	NW rueumorysin; vaccine; pneumonia; meningitis; bacteriaemia; ds. OS Streptococcus pneumoniae
	23-NOV-1990
	R05923;
	ID R05923 standard: protein: 471 AA
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New non:toxic, immunogenic mutants of pneumolysin - useful
protective vaccines against Streptococcus pneumoniae, and I
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                                                                                                                                                                                                                                                                                                                                                                   making them useful in vaccination against pneumonia and associated meningitis, bacteriaemia etc.
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                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; p; English.
Vaccines are non-toxic and antigenic to wild type pneumolysin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WALKER JA;
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15-DEC-1989; AU0539.
16-DEC-1988; AU-001989.
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                                              NSVHSGEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXV
                                                                                                          SSVRGAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDF
                                                                                                                                                                    XVXATXDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSN 120
                                                                                                                                                                                               svtatndsrlypgallvvdetllennptllavdrapmtysidlpglassdsflqvedpsn 120
                                                                                                                                                                                                                              MANKAVNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDI 60
                                                                                                                                                                                                                                                                                           450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATON J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HANSMAN DJ, BOULNOIS GJ, ANDREW PW, MITCHELL
                                                                                                                                                                                                                                                                                                                                                      471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                        94.7%;
                                                                                                                                                                                                                                                                                        Score 2961; DB 1;
Pred. No. 1.08e-248;
5; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                      Length
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a soluble variant of Streptolysin O (SLO) having no haemolytic activity. The variant SLO can specifically recognise wild-type anti-SLO antibodies (ASO) but has no haemolytic activity. It can be used for the determination of previous and/or current infection by Streptococcus pyogenes. It enables ASO assays to become commercially viable and avoids the risk of handling haemo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptolysin O variants produced by recombinant DNA technology having no haemolytic activity and recognised by wild-type anti-streptolysin O antibodies, useful in diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes; ASO. Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLO; soluble;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1993 (first entry)
Streptolysin O variant mSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes infection Claim 17; Fig 2; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 93-100979/12.
N-PSDB; Q38287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1992; U06380.
30-AUG-1991; US-7524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lytically active S. pyogenes wild-type SLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137
   306
                                                                                                                                                                                       257 vfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaaehnkvvtk 316
                                                                                                                                                                                                                                                                                                                                  197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 XDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 indkiyslnynelevlakngetienfvpkegvkkadkfivierkkkninttpvdisiids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIXVXAT 65
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                                  dfdvirnvikdnatfsrknpaypisytsvflknnkiagvnnrteyvettsteytsgkinl 376
                                                                                                                                                                                                                                                                                                                           gekkvmiaaykqifytvsanlpnnpadvfdksvtfkelqrkgvsneapplfvsnvaygrt
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   KVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLL
                                                                                                                                YYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVTG
                                                                                                                                                                                                                                                                    GEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYXRQ
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Similarity 40.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480
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Pred. No. 1.86e-108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 480;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wild-type Streptolysin O
Claim 7; Fig 2; 60pp; English.
The sequence is that of a soluble deriv. of Streptolysin O
with haemolytic properties which was obtd. from Streptococcus pyogenes
genomic library clone rSLO.3. It is useful in immunodiagnostic assays
which rely upon, e.g. the haemolytic properties of wild type
Streptolysin O. Recombinant Streptolysin O is obtd. more cheaply
than purified Streptolysin O obtd. from Streptococcus pyogenes.
Sequence 480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deriv. of streptolysin 0 with haemolytic activity - used in immuno-diagnostic assays which rely on haemolytic activity of wild-type Streptolysin 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble streptolysin O variant.
Recombinant; haemolytic activity; immunodiagnostic activity; ss.
                                                                               366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R33841 standard; Protein; 480
                                                                                                                                                                                                                                                                                                 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JUL-1992; U06398.
30-AUG-1991; US-752429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BECI ) BECKMAN INSTR INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 DHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 43.8%; Local Similarity 40.5%;
                              sectglawewwrkviderdvklskeinvnisgstlsp 473
                                                                                                  shqqayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgansrnirima 436
                                                                                                                                                                                                            VYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVTG 305
                                                                                                                                                                                                                                              vfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaaehnkvvtk 316
                                                                                                                                                                                                                                                                                                                                                        AXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVHS 185
                                                                                                                                                                                                                                                                                                                                                                                         aidnlvnqwhdnysggntlpartqytesmvysksqieaalnvnskildgtlgidfksisk 196
RECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYP 462
                                                                  DHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI 425
                                                                                                                                        KVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLL
                                                                                                                                                                    dfdvirnvikdnatfsrknpaypisytsvflknnkiagvnnrteyvettsteytsgkinl 376
                                                                                                                                                                                                                                                                                  GEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYXRQ
                                                                                                                                                                                                                                                                                                                    gekkvmiaaykqifytvsanlpnnpadvfdksvtfkelqrkgvsneapplfvsnvaygrt 256
                                                                                                                                                                                                                                                                                                                                                                                                                                XDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vtdrtypaalglankgftenkpdavvtkrnpgkihidlpgmgdkat-vevndptyanvst 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIXVXAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rectglawewwrkviderdvklskeinvnisgstlsp 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang EY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1369; DB 6;
Pred. No. 7.25e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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RESULT
ID RO
AC RC
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DE Be
DE St
OS St
FH K¢
FFT C:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KEHO/) KEHOE M.
(PINK/) PINKNEY M.
Kehoe M. Pinkney M;
WPI: 91-024598/04.
                                                                                                                                                                                                                                       R06000 standard; protein; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-1991.
04-JAN-1989;
04-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detecting antibodies in samples detecting antibodies in samples Disclosure; Fig 2; 9pp; English.

The SLO derivative contains no cysteine residues, with cytolytic activity giving resistance to inactivation by oxidation or thiol groups. Abs raised to the SLO may be used in the dection and diagnosis of Streptococcus pyogenes infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; 010320.
Deriv. of thiol-activated protein streptolysin O - contg.
cysteine amino acid but retaining cytolytic activity, use
                                                                                                                                                                                                                                                                                                                                                                         426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes GB2233977-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R10376 standard; Protein; 571 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 DHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptolysin O derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 AXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVHS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 indkiyslnynelevlakngetienfvpkegvkkadkfivierkkkninttpvdisiids 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 vtdrtypaalqlankgftenkpdavvtkrnpqkihidlpgmgdkat-vevndptyanvst 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 XDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIXVXAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLL
                                                                                                                                                                                                                                                                                                                                                                                                   reatglawewwrkviderdvklskeinvnisgstlsp 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shqqayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgansrnirima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaaehnkvvtk 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYXRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aidnlvngwhdnysggntlpartqytesmvysksqieaalnvnskildgtlgidfksisk 287
                                                                                                                                                                                                                                                                                                                                                            RECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 43.6%;
Similarity 40.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1362; DB 2; 1
Pred. No. 3.01e-106;
100; Mismatches 171;
                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   no
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Bacteriophage lambda PL promoter - streptolysin O (SLO) protein of plasmid pMK306. Streptolysin O; SLO; protease; bacteriophage lambda; ds.

cleavage_site

Location/Qualifiers 33..34

Streptococcus pyogenes.

22-NOV-1990

(first entry)

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RESOLLY
ACCOMMENSATION
OF PARTICULAR
OF PART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \mathcal{E}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \mathcal{U}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         raising antibodies, purifying antibodies or detecting antibodies to streptolysin O.
to streptolysin O.
Disclosure; pp; English.
SIO derivative is epitopic to its wild type parent, and may be used in detecting anti-SIO Abs, indicating presence of Streptoco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-1990.
17-NOV-1989; 026008.
18-NOV-1988; GB-027038.
17-NOV-1989; GB-026008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-toxic and non-cytolytic derivs. of streptolysin 0 - used for
                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJC,
Reid RH, Zarfos PN;
WPI; 98-286586/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KEHO/) KEHOE M.
                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1998.
27-OCT-1997; U19226.
01-NOV-1996; US-029930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae encoded polypeptide. coding region; ORF; open reading frame; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W60952 standard; Protein; 113
                                                                                                                                                       e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae
                                                                                                of meningitis
Claim 11; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118
                                The sequence is that of from S. pneumoniae which
                                                                                                                                                                                       New isolated nucleic acids from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9819689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 VRNLSVKIRECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aanpllvgvsakpvngwhdnyspgntlpartgytesmvysksgieaalnvnskildgtlg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              srnirimarectglawewwrkviderdvklskeinvnisgstlsp 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ehnkvvtkdfdvirnvikdnatfsrknpaypisytsvflknnkiagvnnrteyvettste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snvaygrtvfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaa 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       idfksiskgekkvmiaaykqifytvsanlpnnpadvfdksvtfkelqrkgvsneapplfv 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSNSSVRGAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90-217310/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SXVAYXRQVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDFNSVHSGEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRNGDLLLDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ytsgkinlshqgayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgan 319
                                                                                                                                                       for identifying anti-bacterial(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q05240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.1%;
Similarity 42.6%;
   1; Page 53; 130pp; English.

uence is that of the polypeptide encoded by a region isolated pneumoniae which shows homology to pneumolysin. tein, or agonists of it, may be useful as an antibacterial for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=Lambda N promoter - SLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1099; DB 1;
Pred. No. 4.69e-83;
74; Mismatches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 124; Indels
                                                                                                                                                                                       Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                    Lonetto MA,
                                                                                                                                                             for
                                                                                                                                                             treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 371;
                                                                                                                                                                                                                                                                                                                    Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and may be of Streptococcus
                                                                                                                                                             and
                                                                                                                                                             prevention
                                                                                                                                                                                                 useful,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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g Ωy

1 ectglawewwr 11

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427 ECTGLAWEWWR 437

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RESOLLT
ACCORDANCE

PARAMETER

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                                                                                                                                                                                                                       Carmichael E. Spitalny GL, Wu CH, Wu GY, Zhang Y;

RWPI: 96-077502/08.

PSOLUBLE molecular complex for specific targetting of PN to cell -

rinternalises polynucleotide (PN) into endosome, then lyses endosome internalises polynucleotide (PN) into endosome, then lyses endosome to release PN into cell's cytoplasm

Example 3; Page 13; 23pp; English.

Example 3; Page 13; 23pp; English.

City The present peptide is a listeriolysin o (LLO) haemolytic domain the present peptide is a listeriolysin o (LLO) haemolytic domain the present peptide is a listeriolysin o (LLO) haemolytic domain the present peptide is a listeriolysin o (LLO) haemolytic domain the present peptide is a listeriolysin o (LLO) haemolytic domain the present peptide is a listeriolysin o (LLO) haemolytic domain the present peptide in a soluble molecular complex, for the specific targetting of a polynucleotide (PN) to a cell. The complex comprises a PN, a colliber complex ising a pN binding agent and a cell specific binding agent, which binds to a surface mol. of the cell and is internalised into an endosome, and a bacterial component (i.e. the pN into cell's cytoplasm. The complex can be used therapeutically component of a PN to a cell in vivo, ex vivo or in vitro delivery of a PN to a complex can be used the present per cell in the present per cell in the present per cell per cell in the present per cell pe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular it, can also be used in vaccines to induce a cellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeriolysin O; haemolytic; domain; streptolysin O; pneumolysi soluble molecular complex; specific; targetted; polynucleotide; endosome lysis; bacterial component; cytoplasm; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T 8
R88135 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-1994; US-267710.
07-JUN-1995; US-484009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R88135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-1996.
27-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeriolysin
                                                                                                                                                           Sequence
                                                                                                                                                                                                          specific cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in vivo; ex vivo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 RNGDLLLDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCO-) UNIV CONNECTICUT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 rnlrvkiekktgllwnrwqtiyenrpilaqphrkithwgttlnskvsdddv 112
                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.8%;
Similarity 43.2%;
h 3.6%;
Similarity 100.0%;
11; Conservative
                                                                                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in vitro; delivery; cell specific;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
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                                           Score 112; DB 17;
Pred. No. 5.73e+00;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     streptolysin 0; pneumolysin;
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                                                                                 Length 11;
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                     01-FEB-1996; 003649.
01-FEB-1996; DE-003649.
(LUBI/) LUBITZ W.
(SLEY/) SLEYTR U.
KUEN B. LUBITZ W. Sley
WPI: 97-394558/37.
N-PSDB; T75487.
Preparation of S-layer proteins by expressing sbs-A gene in
                                                                                                                                                                                                                                   Bacillus stearothermophilus S-layer protein S-layer; sbs-A; vaccine; adjuvant; carrier;
                                                                                                                             DE19603649-A1.
                                                                                                                                                                                                                      molecular spinning nozzle; molecular laser.
                                                                                                                                                                                                                                                                                         T 10
W22862 standard; Protein; 1228 AA.
                                                                                                                                                                                                            Bacillus stearothermophilus
                                                                                                                                                                                                                                                               27-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 6-7; 12pp; German.

The claimed signal peptide encoding sequence (see tag e of T08695) is pref. operably linked at the 3' end to a protein encoding sequence. The protein is pref. the S-layer protein (see tag f of T08695). At the 5' end, the signal peptide encoding sequence is pref. linked to an expression control sequence, pref. the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding signal peptide of Bacillus stearothermophilus S-layer protein - which has a lysine content of at least 10 per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUL-1994; 425527.
19-JUL-1994; DE-425527.
(VOGE-) VOGELBUSCH GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-layer protein encoded I
sbsA gene; S-layer; cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    given in T08696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus.
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                                                                                                                                                                                                                                                                                                                                                                   314 nipfalntadvslstdgktitvdastpfennteykvvvkgikdkng
                                                                                                                                                                                                                                                                                                                                                                                              260 -EAAFEALIKGVKVAPQTEWKQI-LDNTXVKAVILGGDPSSGARVVTGKVDMVEDLIQEG
                                                                                                                                                                                                                                                                                                                                                                                                                        256 deaaltpkvesvs-aintqnkaveltavpvngt-lklqlsaaanedtvnvntvriykvdg 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYXRQVYLKLETTSXSXEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 yditv-amkar-ev-qdavkagnldkakaavdqinqylpkvtdafktelt-evakkalda 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                           S-RFTADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T08695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                         /label= mat_peptide
                                                                                                                                                                /label=_sig_peptide
                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= sig_peptide
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                                             Sleytr U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 108; DB 17;
Pred. No. 1.06e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
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                                                                                                                                                                                                                                                 sbs-A
                                                                                                                                                                                                                                   hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
    Gram
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Pepitope(s), useful as vaccines and adjuvants

Claim 1; Pages 9-14; 31pp; German.

Chapter protein, sbs-A. S-layer structures can be used as vaccines or adjuvants, particularly when they include a bacterial ghost that can additional epitopes in its membrane. Other uses of crecombinant sbs-A, depending on the nature of the inserted pepide, are as an universal carrier for biotinylated reactants for use in confidence immune responses (epitopes), as a reagent for removing cytokine or toxin from serum (antigenic epitopes), as a molecular cytokine or toxin from serum (antigenic epitopes), as a molecular confidence immune responses (epitopes), as a molecular cytokine or toxin from serum (antigenic epitopes), as a molecular cytokine or toxin from serum (antigenic epitopes), as a molecular cytokine or toxin from serum (antigenic epitopes), as a molecular cytokine or toxin from serum (antigenic epitopes), as a molecular cytokine 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                              by S.pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial gene expression. Detecting a sequence encoding the protein can be used diagnostically, e.g. to detect a mutation for
                     serotyping
                                                                                                                                                                                                                                                                                                                        The sequence is that of the polypeptide encoded by a region isolated from S. pneumoniae which shows homology to nicotinate nucleotide pyrophosphorylase. It, or agonists of it, may be useful as an antibacterial for treatment or prevention of infection, specifically caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. for ident
of meningitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acids from Streptococcus pneumoniae e.g. for identifying anti-bacterial(s) for treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-1997; U19226.
01-NOV-1996; US-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae encoded polypeptide coding region; ORF; open reading frame; antil
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 71-72; 130pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; V3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. Black MT, Hodgson JE, Knowles DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W60976 standard; Protein; 299 AA W60976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; prevention; meningitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 S-RETADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 nipfalntadvslstdgktitvdastpfennteykvvvkgikdkng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%;
Local Similarity 23.5%;
les 39; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98-286586/25.
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299
               or classifying infectious agents
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Claim 4; Page 53-57; 94pp; Japanese.

Vectors containing DNA fragments encoding proteins of plant origin with aromatic acyl transferase activity may be used to transform plants which produce anthocyanin pigments. The aromatic acyl transferase acylates the pigments in the flower resulting in colour tone changes and allowing new colourations to be produced. Six specific DNA sequences encoding aromatic acyl transferase from different plants are described in T37308-T37313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scenecio cruentus; Lavandula angustifolia.
Gentiana triflora var. japonica (Clone pGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gentiana triflora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aromatic acyl transferase of Gentiana triflora var. japonica Aromatic acyl transferase; transformation; anthocyanin pigme plants; acylation; colour; tone; colouration; colour change;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W04722;
06-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA coding for aromatic acyl transferase - for transforming plants which produce anthocyanin pigments and thus altering colour tone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-FEB-1996; J00348.
17-FEB-1995; JP-067159.
29-JUN-1995; JP-196915.
30-JAN-1996; JP-046534.
               17-JUN-1998 (first entry)

H. pylori ORF Olcel16.Borf11 protein.

Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakao
                                                                                                           w55347 standard; Protein; ws5347;
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 Helicobacter pylori
                                                                                                                                                                                                                                209 sfdrsiikdlygleetfwne-mgdvlemfsrfgskpprfnkv 249
                                                                                                                                                                                                                                                                    204 VDAVKNPGDVFQDTVTVEDLK-QRGISAERPLV-YISXVAYXRQVYLKLETTSXSXEVEA 261
                                                                                                                                                                                                                                                                                                    151 iplvavqvtvfpnrgiavaltahhsiadaksfvmfinawayink-fgk-dadllsanllp 208
                                                                                                                                                                                                                                                                                                                                          146 ARXQYEKXTAHSMEQLKVKFGSDFE-KXGNSLDIDFNSVHSGEKXI-QIVNXKQIYYTVS 203
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                                                                                                                                                                                                262 AFE-ALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kari T, Fujiwara H, Fuk
o M, Tanaka Y, Yonekura
96-393401/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of flowers
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Similarity 19.8%;
32; Conservation
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llarity 20.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petunia hybrida; Perilla ocimoides;
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                                                                                                                            188 AA
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Pred. No. 2.63e+01;
33; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   49;
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Pred. No. 2.63e+01;
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Helicobacter pylori nucleic acid sequences and encoded PT Helicobacter pylori nucleic acid sequences and encoded PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori PT infection and for diagnosis of H. pylori infection PS Claim 14; Page 571; 1145pp; English.

CC This sequence is a H. pylori protein of unspecified function. PS Claim 14; Page 571; 1145pp; English.

CC The protein may be used in a vaccine to prevent or treat H. pylori protein of unspecified function. On the infection or to identify H. pylori polypeptide binding compounds, infection or to identify H. pylori polypeptide binding compounds. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC acid sequences complementary to the DNA act as antisense sequences and CC acid sequences complementary to the DNA act as antisense sequences and CC and distribution of H. pylori-specific antigens. The genomic sequence of CC H. pylori (ANCC 55679) was determined from overlapping contigs generated CC by mechanically shearing the bacterial DNA. The sequences were analysed for or ore of at least 180 nucleotides, and the predicted coding regions CC defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various or contigues of interest, particular regions can be isolated from H. pylori by PCR interest, particular regions can be isolated from H. pylori by PCR interest, particular regions can be isolated from H. pylori by PCR interest, particular regions can be isolated from H. pylori by PCR interest.
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   RESULT
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09-OCT-1997.
27-MAR-1997; U06-DEC-1996; U06-
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02-APR-1996;
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Alm RA, Smith D;
WPI; 97-503122/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1998 (first entry)
H. pylori ORF 29ge30321_24336712_f1_5 cellular protein.
                                                                                       (ASTR ) ASTRA AB.
Alm RA, Smith D;
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06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                    W09737044-A1
                                                                                                                                                                                                                                                                                                                                                                                                               inhibitor; duodenal ulcer disease;
Helicobacter pylori.
                              N-PSDB;
                                                                                                                                                          28-OCT-1996;
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                                                            97-503122/46.
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US-625811.
US-758731.
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US-761318.
US-625811.
US-758731.
US-736905.
US-738859.
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pylori nucleic acid sequences and
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Pred. No. 3.05e+01;
20; Mismatches 18
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          encoded
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IRESULT
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S Claims 14,93; Page 730-731; 1145pp; English.

CC This sequence is a H. pylori cellular protein.

CC The protein may be used in a vaccine to prevent or treat H. pylori

CC infection or to identify H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors. The

CC DNA and probes derived from it may be used for the identification of

CC acid sequences complementary to the DNA act as antisense sequences and

CC acid sequences complementary to the DNA act as antisense sequences and

CC can be used to prevent the translation of H. pylori inRNA. Antibodies

CC and distribution of H. pylori-specific antigens. The genomic sequence of

CC and distribution of H. pylori-specific antigens. The genomic sequence of

CC by mechanically shearing the bacternial DNA. The sequences were analysed

CC defined by computer evaluation. To identify likely H. pylori antigens for

vaccine development, the amino acid sequences predicted from various ORF

vaccine development, the anino acid sequences predicted from various ORF

cc amplification for recombinant nolvpentide mroduction. An in F. Coli
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Best Local Similarity 32.8%;
Matches 20; Conservative
               Claim 24; Page 25; 112pp; English.

The sequences given in Q50429-33 may be used for the detection of MTP or MTP inhibitors.

Bovine and human MTP are useful for the prevention, stabilisation or regression of atherosclerosis or for lowering the level of serum lipids such as serum cholesterol, triglyceride, phosphatidyl choline or cholesteryl ester in a mammalian species.

Diseases associated or affected by serum lipid levels, such as pancreatitis, hyperglycemia, obesity, etc., may be treated.
                                                                                                                                                                                                                                                                                                                                                       Nucleic acid sequence encoding sub-unit of MTP - used to express polypeptide for therapeutic use e.g. in reduction of obesity atherosclerosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SQUI) SQUIBB & SONS INC E R. (WETT/) WETTERAU J R. Gregg RE, Sharp DY, Wetterau JR; WPI: 93-337295/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTP; microsomal triglyceride transfer protein; obesity; atherosclerosis; detection; inhibitor; prevention; stabilisation; regression; lipid; serum cholesterol; SC; triglyceride; TG; phosphatidyl choline; PC; cholesteryl ester; CE;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Q50429.
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06-MAR-1992; US-847503
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       860 AA;
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Query Match

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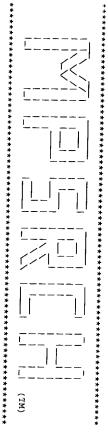
Length 860

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161 LKVKF-GSDFEKXGNSLDIDFNSVHSGE-KXIQIVNXKQ 197
                                599 ldilysgsgilrrsn-lni-fqyiektplhgiqvvieag 635
                                                                   103 LPGLASSDSFLQVEDPSNSSVRGAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQ-- 160
                                                                                                    541 m--lsivqdilrfetpaskmvrqvlkemvahnydrfsksgssaytgyvertshsastys 598
                                                                                                                                                                            481 fitdevkktmnriyhqnrkihektvrttaaaiilknnpsymevknillsigelpkemnky 540
                                                                                                                                           43 FVXXERKKRSLSTNTSDIXVXATXDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXX 102
                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                            larity 20.1%;
Conservative
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Search completed: Mon Aug 30 16:15:24 1999 Job time: 80 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 30 16:12:54 1999; MasPar time 20.74 Seconds 909.898 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-09-120-044-4 (1-471) from US09120044.pep 3127

Sequence: 1 MANKAVNDFILAMNYDXXKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 50.051; Variance 108.607; scale 0.461

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21 22 23	11 12 13 14 15 16 17 18	1 1 1 1 1 1 1 1 1 1	Result
105 105 102	209 113 112 114 109 108 108	3127 1556 1475 1468 1460 1416 1416 1379 1298	Score
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776 780 365	265 265 527 744 1361 1218 462 1228 364	471 500 529 528 528 501 501 530 571 485	Query Match Length
221	2221232222	00000000000	BB
RGECAR S77652 F71665	S47297 S60947 S60947 A70385 T03415 T64461 S60468 JC1188 A70444	A28568 B43577 A43505 S24231 S22341 S22341 A37858 S22340 A43507 I39863 S47298	ID
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ALIGNMENTS

Db 61 SVTAT Qy 61 XVXAT	Db 1 MANKA Qy 1 MANKA	Query Match Best Local Si Matches 445	2-471 SUMMARY	##residues ##cross-re CLASSIFICATION FEATURE	##Status ##molecule_type	#accession	#title	#journal	#authors	REFERENCE	##molecul	#accession	#cross-refe	#title	#journal	#authors	ACCESSIONS	DATE	ORGANISM	ENTRY	RESULT 1
SVTAINDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSN 120 	MANKAVNDFILAMNYDKKKLLTHQGESIENREIKEGNQLPDEFVVIERKKRSLSTNTSDI 60 	Query Match 100.0%; Score 3127; DB 2; Length 471; Best Local Similarity 94.5%; Pred. No. 0.00e+00; Matches 445; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	#product pneumolysin #status predicted #label MAT #length 471 #molecular-weight 52899 #checksum 8274	feren #sup	preliminary e_type DNA	accession \$12829	Comparison of pneumolysin genes and proteins from Streptococcus pneumoniae types 1 and 2.	Nucleic Acids Res. (1990) 18:4010	Mitchell, T.J.; Mendez, F.; Paton, J.C.; Andrew, P.W.;	S12829	##molecule_type DNA	A28568	sulfhydryl-activated toxin of Streptococcus pneumoniae.	Molecular cloning, characterization, and complete nucleotide	Bouinois, G.J. Infect. Immun. (1987) 55:1184-1189	Walker, J.A.; Allen, R.L.; Falmagne, P.; Johnson, M.K.;	A26568; S12829	19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change	#formal name Streptococcus pneumoniae	A28568 #type complete	

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                                                                                   FEATURE
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#title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #authors Tweten, R.K.

#journal Infect. Immun. (1988) 56:3235-3240

#title Nucleotide sequence of the gene for perfringolysin O

#totheta-toxin) from Clostridium perfringens: significant
homology with the genes for streptolysin O and pneumoly:
#cross-references_MUID:89032623
                                                                                                                                                                                                                                  perfringens and characterization #cross-references MUID:89032622
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                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-125,'EA',129-500 ##label TWE ##cross-references GB:M36704; NID:g144883; PID:g144884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-500 ##label SHI
##cross-references GB:M81080; NID:g144885; PID:g144886
##note translation of the nucleotide sequence is not complete
                                                                                                                                              ##molecule_type protein
##residues 29-45 ##label TW2
##experimental_source ATCC 13124
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Shimizu,
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perfringolysin O precursor - Clostridium perfringens
#formal_name Clostridium perfringens
03-Feb-1993 #sequence_revision 03-Mar-1993 #text_change
                                                                                                                                                                                                                                                             Cloning and expression in Escherichia coli of the perfringolysin O (theta-toxin) gene from Clostridium perfringens and characterization of the gene product.
                                                                                                                                                                                                                                                                                                                      Tweten, R.K.
Infect. Immun. (1988) 56:3228-3234
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#length 500
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                                      #domain signal sequence #status predicted #label SIG\
#product perfringolysin O #status experimental #label
#molecular-weight 55799
    #checksum 4821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 VANNEKKVMILAYKQIFYTVSADLPKNPSDLFDDSVTFNDLKQKGVSNEAPPLMVSNVAY 273
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                                                                                                                                                                                                                                                                                                                                    ##residues 1-529 ##label MEN
##cross-references GB:M24199; NID:g149652; PID:g149653
##note this sequence is derived from a strong
                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
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Local Similarity 45.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                         ##status
                                                                ##cross-references EMBL:X15127; NID:g44106; PID:g44107
##experimental_source strain EGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.C.; Cossart, P.
Infect. Immun. (1988) 56:766-772
Expression in Escherichia coli and sequence analysis of the
listeriolysin O determinant of Listeria monocytogenes.
                                                                                                                                                                                                                         Domann, E.; Chakraborty, T.
Nucleic Acids Res. (1989) 17:6406
Nucleotide sequence of the listeriolysin gene
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Geoffroy, C.; Gicquel-Sanzey, B.; Baquero, F.; Perez-Di
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listeriolysin O precursor - Listeria monocytogenes
#formal_name Listeria monocytogenes
21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change
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                                                this sequence is derived from a weakly hemolytic strain
                                                                                                                 1-529 ##label DOM
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Pred. No. 3.55e-265;
99; Mismatches 151;
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                                                                                                                          425 IRECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYPQVEDKVEN
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Local Similarity 40.8%;
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                                                                                                                                                                                                                    LDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
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       S24231 #ty
listeriolysin
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Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtained by single amino acid substitutions in listeriolygin O.
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Identification of the structural gene encoding the
SH-activated hemolysin of Listeria monocytogenes:
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monocytogenes (strain
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#accession S24231
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                                                                                                                                                                        481 AKECTGLAWEWWRTVIDDRNLPLVKNRNISIWGTTLYPKYSNSVDN 526
                                                                                                                                                   425 IRECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYPQVEDKVEN 470
                                                                                                                                                                                                                                365 LDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
                                                                                                                                                                                                                                                                          421 IDHSGGYVAQFNISWDEINYDPEGNEIVQHKNWSENNKSKLAHFTSSIYLPGNARNINVY 480
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                                                                                                                                                                                                                                                                                                                                                                                                        245 QVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVT 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-529 ##label RAS ##cross-references EMBL:X60035; NID:g44110; PID:g44112 ##experimental_source strain 12067, serotype 4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AVNTLVERWNEKYAQAYPNVSAKIDYDDEMAYSESQLIAKFGTAFKAVNNSLNVNFGAIS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
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Similarity 40.6%;
$22341 #type complete ivanolysin precursor - Listeria #formal_name Listeria ivanovii 07-Apr-1994 #sequence_revision
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strain 12067
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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#th 529 #molecular-weight 58687 #checksum 47
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Pred. No. 4.04e-248;
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                                          Listeria ivanovii
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Local Similarity 40.8%;
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Biochim. Biophys. Acta (1992) 1130:81-84
Listeriolysin genes: complete sequence of ilo from Listeria
ivanovii and of 1so from Listeria seeligeri.
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#product ivanolysin #status predicted #label MAT
#length 528 #molecular-weight 58511 #checksum 6874
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alveolysin - Bacillus alvei
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28-Jun-1991 #sequence_revision 28-Jun-1991
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                                                               ##cross-references EMBL:X60462; NID:g44144; PID:g44145
##note the authors translated the codon GCC f
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J. Bacteriol. (1990) 172:7301-7305
Alveolysin, the thiol-activated toxin of Bacillus alvei,
homologous to listeriolysin O, perfringolysin O,
pneumolysin, and streptolysin O and contains a single
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                                                                                                                                                                                                        Haas, A.; Dumbsky, M.; Kreft, J.
Biochim. Biophys. Acta (1992) 1130:81-84
Listeriolysin genes: complete sequence of ilo from Listeria
ivanovii and of lso from Listeria seeligeri.
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seeligeriolysin - Listeria seeligeri
#formal_name Listeria seeligeri
22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change
#superfamily #length 530
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228 AIDNLVNOWHDNYSGGNTLPARTQYTESMVYSKSQIEAALNVNSKILDGTLGIDFKSISK 287
                                                                                                                                                                                                       109 INDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIERKKKNINTTPVDISIIDS 168
                                                                                                                                                                                                                                                                                                                                         ##residues 1.571 ##label KEH
##cross-references GB:M18638; NID:g153810; PID:g153811
## #length 571 #molecular-weight 63638 #checksum
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##resider
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                                                                                                            169 VTDRTYPAALQLANKGFTENKPDAVVTKRNPQKIHIDLPGMGDKAT-VEVNDPTYANVST 227
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                                                                 66 XDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVRG 125
                                                                                                                                                                                                                                                     V Match 44.1%; Score 1379; DB 2; L
Local Similarity 40.7%; Pred. No. 6.61e-231;
nes 186; Conservative 100; Mismatches 170;
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Local Similarity 40.6%; Pred. No. 1.14e-237;
hes 189; Conservative 109; Mismatches 167; Indels
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                                                                                                                                                            6 VNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIXVXAT 65
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streptolysin Oprecursor - Streptococcus pyogenes
#formal_name Streptococcus pyogenes
28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors
                        343 KDFNEIRNIIKDNAELSFKNPAYPISYTSTFLKDNATAAVHNNTDYIETTTTEYSSAKMT 402
                                                                                                                                                                                                                                                                               125 GAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ##residues 1-485 ##label RES
##cross-references GB:D21270; NID:g418066; PID:g600252
## #length 485 #checksum 3782
                                                                                                                                      283 TVYVKLETTSKSKDVQAAFKALLKNNSVETSGQYKDIFEESTFTAVVLGGDAKEHNKVVT 342
                                                                                                                                                                                     185 SGEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYXR 244
                                                                                                                                                                                                                                  223 NGEKKVMVAAYKQIFYTVSAELPNNPSDLFDNSVTFGELTRKGVSNSAPPVMVSNVAYGR 282
                                                                                                                                                                                                                                                                                                                           163 GAVDDLVSTWNEKYSATHTLPARMQYTESMVYSKAQIASALNVNAKYLDNSLNIDFNAVA 222
                                                                                                                                                                                                                                                                                                                                                                                                                          104 SVANRTYPGAVQLANKAFADNQPSLLVAKRKPLNISIDLPGMRKENT-ITVQNPTYGNVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                65 TXDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 SIDTGIGNLTYNNQEVLAVNGDKVESFVPKESINSNGKFVVVDVRKNHLQRHQSIFRLLD 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                         QVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 41.5%; Score 1298; DB 2; I
1 Similarity 38.4%; Pred. No. 2.84e-215;
167; Conservative 113; Mismatches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Minamide, W.; Igarashi, H.; Hinuma, Y.
Infect. Immun. (1994) 62:4000-4004
The gene encoding a new mitogenic factor in a Streptococcus pyogenes strain is a distributed only in group A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I39863 #type fragment
hemolysin - Bacillus cereus (fragment)
#formal_name Bacillus cereus
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
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Yutsudo, T.; Okumura, K.; Iwasaki, M.; Hara, Y.
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Best Local Similarity 32.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ##residues 1-112 ##label SEG
##cross-references EMBL:Z36908; NID:g535307; PID:g535308
## #length 112 #molecular-weight 12464 #checks
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##cross-references EMBL:236907; NID:g535305; PID:g535306
# #length 96 #molecular-weight 10471 #checksum 6662
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                                                                                                                   64 ATXDSRLYPGALLVVDETXLENNPTLLAV
                                                                                                                                                           61 XAKAANISPGALLRAXQNLLDNNPTLISI 89
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                                                                                                                                                                                                   4 KAVNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIXVX 63
                                                                                                                                                                                                                                         1 KQDNQYFQSLTYGPQEILINEGEYIDNPPATTGMLENGRFVVLRREKXTITDNSADITVI 60
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#formal_name Streptococcus suis
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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S47297
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#formal_name Streptococcus suis
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
                hypothetical protein YOR220w - yeast (Saccharomyces
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                                                                 #authors Powell, J.F.; Hsu, Y.P.P.; Weyler, W.; Chen, S.; Salach, Andrikopoulos, K.; Mallet, J.; Breakefield, X.O.
#journal Biochem. J. (1989) 259:407-413
#title The primary structure of bovine monoamine oxidase type A.
Comparison with peptide sequences of bovine monoamine oxidase type B and other flavoenzymes.
#cross-references_MUID:89246344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #authors Galisson, F.; Dujon, B.
Yeast (1996) 12:877-885
#title Sequence and analysis of a 33 kb fragment from the right arm
c chromosome XV of the yeast Saccharomyces cerevisiae.
#cross-references MUID:96437977
#accession $71722
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##cross-references EMBL:Z75128; N
MIPS:YOR220w
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##note the nucleotide sequence was submitted to the EMBL Data
Library, October 1995
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NCE $71713
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##molecule_type mRNA
                           ##status
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Local Similarity 35.2%;
les 25; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 FVXXERKKRSLSTNTSDIXVXATXDSRLY-PGALLVVDETXLENNPTL-LAVDRAPMTYS 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galisson, F.; Dujon, B. submitted to the EMBL Data Library, October 1995 seguence and analysis of a 33 kb fragment from the right arm of chromosome XV of the yeast Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S60947
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$60938
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                                                                                                                                                                                                                                                                                                                                                                                       $03974 #type complete amine oxidase (flavin-containing) (EC 1.4.3.4) A - bovine
                                                  S03974
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                           not compared with
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                           conceptual translation
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Matches 28; Conservative
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                                                                                                                                                      449 IEY-YKKLVASEGERI-KVFIEETEELVKKY--GD-KRRTFIGGVKEVKEGSITVAVLQD 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 GSIIPVEELPLEKAP-VVNILRVPFTEGLFL 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ##molecule_type DNA
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##cross-references GB:X15609; NID:g523; PID:g524
RDS FAD; flavoprotein; mitochondrion; oxidoreductase
                                                                                                                                                                                                                             Local Similarity 24.2%; nes 22; Conservation
                                                                           13 MNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIXVXATXDSRLYP 72
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Nature (1998) 392:353-358
The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                           #domain phage T4 DNA topoisomerase (ATP-hydrolyzing)
medium chain homology #label TOP
#length 744 #molecular-weight 84080 #checksum 7466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #superfamily DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain
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A70300
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DNA gyrase A subunit - Aquifex aeolicus
#formal_name Aquifex aeolicus
08-May-1998 #sequence_revision 08-May-1998 #text_change
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                                                                                                                                                                                                                                 Score 112; DB 2; Length 744; Pred. No. 3.63e-01; 26; Mismatches 37; Indels
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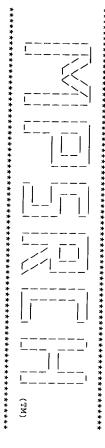
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                                                                                                                                                                                237 NTLNVEFGQANADEGDPTSRTPTLTNIQNINIEVTGTVNTLDL-RDSNDVEKINIHRITK 295
                                                                                                                                                                                                                        115 VEDPSNSSVRGAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSME-QLKVKFGSDFEKXG 173
                                                                                                                                                                                                                                                            178 VDWHSNPEHPGKAYELTINTDNATANVFNAPMK-HNPGGTDRIMTLQSSDKLTGDYSRHD 236
                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-1361 ##label WAN ##cross-references EMBL:AFC10143; NID:92459960; PID:92459961;
                                       353 LSITSD 358
                                                                                                                                               174 NSLDIDENSVHS--GEKXIQIVNXKQI-YYTVSVDAVKNPGDVFQDTVTVEDLKQRGISA 230
   290 VILGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##status
                                                                                                                                                                                                                                                                                                        / Match
Local Similarity 19.9%;
les 37; Conservative
                                                                                                         EAGNKFNVESIG-QKLVGMRLANVAK-KDIDVKFEH-KKGVLSGFEDKSNVFLENVEAKS
                                                                         ERPLVY-ISXVAYXRQVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKA
   295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang, B.; Kraig, E.; Kolodrubetz, D.
Infect. Immun. (1998) 66:1521-1526
A new member of the S-layer protein family: characterization
of the crs gene from Campylobacter rectus.
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S-layer protein - Campylobacter rectus
#formal_name Campylobacter rectus
16-Mar-1999 #sequence_revision 16-Mar-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                 PID:g2459961 #length 1361 #molecu
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Pred. No. 2.11e-01;
50; Mismatches 89;
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Search completed: Mon Aug 30 16:13:46 1999 Job time: 52 secs.

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Suc on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Mon Aug 30 16:10:12 1999; MasPar time 14.42 Seconds 923.239 Million cell updates/sec

Tabular output not generated. Title:

Description: Perfect Score: >US-09-120-044-4 (1-471) from US09120044.pep 3127 1 MANKAVNDFILAMNYDXXKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 51.211; Variance 95.336; scale 0.537

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
ъ	3116	99.6	470	_	TACY STRON	, :	
2	1556	49.8	500	,	۲,	PERFRINGOLYSIN O PRECII	0.000+00
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υ	1416	45.3	501	ட	TACY PAEAL	ALVEOLYSIN PRECURSOR	4 14C-377
ı on	1414	45.2	530	ب	TACY_LISSE	SEELIGERIOLYSIN PRECIE	1 176-276
7	1379	44.1	571	Н	TACY_STRPY	STREPTOLYSIN O PRECURS	8 800-260
, cc	1380	44.1	574	ب	TACY_STREQ	0	5.246-269
, 40	1363	43.6	574	μ.	TACY_STRCB	0	3.49e-265
1 ← 1 ←	9677	⊥	4 1	· -	TACY_BACCE	HEMOLYSIN PRECURSOR (F	1.40e-250
	2 F	٠	527	-	AOFA_BOVIN	AMINE OXIDASE [FLAVIN-	.96e-02
1 1	108	ن ن	462	Н	MPPB_YEAST	MITOCHONDRIAL PROCESSI	.34e-0
1 L	100		1228	ч	SLAP_BACST	S-LAYER PROTEIN PRECUR	.34e-0
_	100		1004	۰ -	GCH2_PHOLE	GTP CYCLOHYDROLASE II	.15e-0
1 L	100		776	· -	ARCB_ECOLI	AEROBIC RESPIRATION CO	.67e-
1 to	105		780	-	CTPA_MYCLE		e-0
· -	707	•	514	۳	THD1_SALTY	Ω.	ω.
, L	103	•	722	щ	YG42_YEAST	HYPOTHETICAL 78.8 KD P	1.01e+00
) <u>L</u>	Z07		878	Н	SYV_METJA	ASE	
, ,		٠.	2/9	Н	YRR6_MYCCA	HYPOTHETICAL 33.0 KD P	3.14e+00
17	TOT	3.2	350	Н	ARGI_SOYBN		
22	100	3.2	427	μ	GLYA_SYNY3	DRC	2.38e+00
23	100	3.2	502	Н	SPE1_LYCES	ARGININE DECARBOXYLASE	

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ALIGNMENTS

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Query Match 99.6%; Score 3116; DB 1; Length 470; Best Local Similarity 94.5%; Pred. No. 0.00e+00;	ESTEROL (BY SIM	produced through a collaborati atics and the EMBL outstation here are no restrictions on i as its content is in no wd. Usage by and for commercie http://www.isb-sib.ch/announce	1987). IVATED TOXIN. IS ABLE TO LYSE CHOLEST IVATED TOXINA. N BE REVERSIBLY INACTIVATED BY OXIDAR TOR FOR THE BINDING OF THESE TOXINS TO S. S. TOTAL ACTIVATED CYTOLYSIN FAMILY.	DENCH AIN=N LINE; KER J Lecul Lecul	STREPTOCOCCUS PNEUMONIAE. BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; STREPTOCOCCUS. [1]	01-CCT-1989 (REL. 12, CREATED) 01-CCT-1989 (REL. 12, LAST SEQUENCE UPDATE) 15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE) PNUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN).	RESULT 1 ID TACY_STRPN STANDARD; PRT; 470 AA. AC P11990:

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01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PERFINENCIASIN O PRECURSOR (THETA-TOXIN) (THIOL-ACTIVATED PEO OR PEOR OR PEOA.
                     MEDLINE: 87076517.

OHNO-IWASHITA: I WAMOTO M., MITSUI K., KP
"Cold-labile hemolysin produced by limited
from Clostridium perfringens.";
BIOCHEMISTRY 25:6048-6053(1986).
                                                                                                                                                                                                                                  "An upstream regulatory sequence stimulates expression of the perfringolysin O gene of Clostridium perfringens."; INFECT. IMMUN. 59:137-142(1991).
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                                                                                                                              "Nucleotide sequence of the gene for perfringolysin O (theta from Clostridium perfringens: significant homology with the streptolysin O and pneumolysin."; INFECT. IMMUN. 56:3235-3240(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Structure of a cholesterol-binding, thiol-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
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            154 VSGAIDELVSKWNEKYSSTHTLPARTQYSESMYYSKSQISSALNVNAKVLENSLGVDFNA
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SUBUNIT: FORMS OLIGOMERS IN THE HOST MEMBRANE.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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                                                                                                                                                                                                                   BINDING TO CHOLESTEROL.
D -> K (IN REF. 3).
K -> I (IN REF. 3).
RKP -> EA (IN REF. 2).
RKP -> EA (IN REF. 2).
                                                                                                                                                            score 1556; DB 1; I
Pred. No. 0.00e+00;
99; Mismatches 151;
                                                                                                                                                                                                                                                                                                                           SIGNAL; PLASMID;
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                                                                                                                                                                                                                                                                                               PERFRINGOLYSIN
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s of a thiol-activated
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration hetween the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                 STRAIN-F2365, F5782 (SEROTYPE 4B), AND F4233, F6789 (SEROTYPE 1/2B);
                                                                                                                                                                                                                                 RASMUSSEN O.F., BECK T., OLSEN J.E., DONS L., ROSSEN L.; "Listeria monocytogenes isolates can be classified into two types according to the sequence of the listeriolysin gene."; INFECT. IMMUN. 59:3945-3951(1991).
                                                                                                                                                                                                                                                                                                                                                     MENGAUD J., VICENTE M.-F., CHENEVERT J., PEREIRA J.M., GEOFFI GICQUEL-SANZEY B., BAQUERO F., PEREZ-DIAZ J.-C., COSSART P., "Expression in Escherichia coli and sequence analysis of the listeriolysin O determinant of Listeria monocytogenes."; INFECT. IMMUN. 56:766-772(1988).
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P13128; Q48747; Q57906; Q57206;
01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
LISTERIOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
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                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMANN E., CHAKRABORTY T.;
"Nucleotide sequence of the listeriolysin monocytogenes serotype 1/2a strain.";
mucleic ACIDS RES. 17:6406-6406(1989).
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EMBL; M24199; G149653; -..
EMBL; X60035; G44112; -..
EMBL; U25452; G887870; -..
EMBL; U25443; G887016; -..
EMBL; U254446; G887028; ALT_INIT.
EMBL; U25449; G887864; ALT_INIT.
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                                                               481 AKECTGLAWEWWRTVIDDRNLPLVKNRNISIWGTTLYPKYSNKVDN 526
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PIR; A43505; A43505.
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                                    IRECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYPQVEDKVEN 470
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                                                                                             LDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
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BINDING TO CHOLESTEROL (BY SIMILAR: S-> L (IN STRAINS F2365, F4233, F)
F6789 AND 12067).

M -> I (IN STRAIN F2365, F4233, F)
V -> I (IN STRAIN F2365, F4233, F)
F6789 AND 12067).
X -> S (IN STRAINS F2365, F4233, F)
F6789 AND 12067).
F6789 AND 12067).
F6789 AND 12067).
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Pred. No. 2.10e-290;
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55, F4233, F5782,
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(REL.

26, CREATED)
26, LAST SEQUENCE UPDATE)
36, LAST ANNOTATION UPDATE)

TACY_LISIV P31831;

STANDARD;

528

AA

IVANOLYSIN PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).

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SOURCE REPRESENTATION OF SOURCE REPRESENTATION
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LISTERIA IVANOVII.
BACTERIA; FIRMICUT
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SEQUENCE
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BIOCHIM. BIOPHYS. ACTA 1130:81-84(1992).
-i- FUNCTION: SULPHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
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HSSP; P19995; 1PFO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIFVKLSTSSHSTRVKAAFDTAFKGKSVKGDTELENIIQNASFKAVIYGGSAKDEVEIID 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGKVQEEVINFKQIYYTVNVNEPTSPSRFFGKSVTKENLQALGVNAENPPAYISSVAYGR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AXXDLLAKWHQDYGQVN-NVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVH
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                                                                                                                                                                                              LDHSGAYVARFNVTWDEVSYDANGNEVVEHKKWSENDKDKLAHFTTSIYLPGNARNINIH 479
                                                                                                                                                                                                                                                                                                                                                                                                    QVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVNTLVDRWNNKYSEEYPNISAKIDYDQEMAYSESQLVAKFGAAFKAVNNSLNVNFGAIS 239
                                                                                                                                                                                                                                                                       GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
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      IRECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYPQVEDKVEN 470
                                                                 AKECTGLAWEWWRTVVDDRNLPLVKNRNVCIWGTTLYPAYSDTVDN 525
                                                                                                                                       LDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189;
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Similarity 40.6%;
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483
528 AA;
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483 B
; 58542 MW;
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Pred. No. 1.43e-286;
117; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING TO CHOLES; CFAE84AD CRC32;
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Best Local
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P23564;
01-NOV-1991 (REL. 20, C
01-NOV-1991 (REL. 20, I
15-DEC-1998 (REL. 37, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEOFFROY C., MENGAUD J., ALOUF J.E., COSSART P.;
"Alveolysin, the thiol-activated toxin of Bacillus alvei, is
"homologous to listeriolysin O, perfringolysin O, pneumolysin,
streptolysin O and contains a single cysteine.";
J. BACTERIOL. 172:7301-7305(1990).
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15-DEC-1998 (REL. 37, LAST ANNOTATION UPDAT
ALVEOLYSIN PRECURSOR (THIOL-ACTIVATED CYTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALOUF J.E., GEOFFROY C., GILLES A.M., FALMAGNE P.,
(IN) RAPPUOLI R., ALOUF J.E., FALMAGNE P. (EDS.);
BACTERIAL PROTEIN TOXINS, PP.49-50, GUSTAV FISHER
STUTTGART (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 91072294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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  190
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                                                                                                                                                                                                                                                                 163
                                                                                                                                                                                                                                                                                                                                                                         104 TYPGAIQLANKDFADNQPSLVMAARKPLDISIDLPGLKNENT-ISVQNPNYGTVSSAIDQ
                                                                                                                                                                                                                                                                                                                   70 LYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVRGAXXD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 IAGLNYNRNEVLAIOGDQISSFVPKEGIQSNGKFIVVERDKKSLTTSPVDISIVDSITNR 103
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                                                                                                                                         VMVAAYKQIFYTVSAGLPNNPSDLFDDSVTFAELARKGVSNEAPPLMVSNVAYGRTIYVK
                                                                                                                                                                                                                                                              LVSTWGEKYSSTHTLPARLQYAESMVYSQNQISSALNVNAKVLNGTLGIDFNAVANGEKK
                                                                                                                                                                                                     LLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVHSGEKX 189
                                                                                         IQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYXRQVYLK
HEMOLYSIS; CYTOLYSIS; SIGNAL
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461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1416; DB 1;
Pred. No. 4.14e-277
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A -> L (IN REF. 2).
; 8DF2C94A CRC32;
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GUSTAV FISHER VERLAG.
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SEQUENCE
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PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
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                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                      PFAM; PF01289;
HSSP; P19995; 1
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X60462; G44145; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Listeriolysin genes: complete sequence of ilo from Listeria ivanovii and of 1so from Listeria seeligeri";
BIOCHIM. BIOPHYS. ACTA 1130:81-84(192).
182 AVNTLVERWNDKYSKAYPNINAKIDYSDEMAYSESOLIAKFGTAFKAVNNSLNVNFEAIS 241
                                                                                                                                                                                                                                                                                                                 TOXIN; HEMOLYSIS; CYTOLYSIS; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEELIGERIOLYSIN PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                            122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-JUL-1993
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                                              66 XDSRLYPGALLVYDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVRG 125
                                                                                                                                            62 INKYIWGLNYDKNSILVYQGEAVTNVPPKKGYKDGSEYIVVEKKKKGINQNNADISVINA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 GLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYP 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 LETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVTGKVDM 309
                                                                                                                                                                                                       Local
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                                                                              ISSLTYPGALVKANRELVENQPNVLPVKRDSLTLSVDLPGMTKKDNKIFVKNPTKSNVNN 181
                                                                                                             VNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIXVXAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTIC CELL MEMBRANES
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                                                                                                                                                                                                  h 45.2%; Score 1414; DB 1; Similarity 40.6%; Pred. No. 1.17e-276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DUMBSKY M., KREFT J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92182018
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                                                                                                                                                                                                                                                     530 AA;
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(REL. 26, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                        1PFO
                                                                                                                                                                                                                                                                                                                                               Thiol_cytolysin; 1.
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                                                                                                                                                                                                                                                     59181 MW;
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                                                                                                                                                                                                                                                                  BINDING
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                                                                                                                                                                                                                                                   INDING TO CHOLESTEROL (BY SIMILARITY).
68A497A5 CRC32;
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                                                                                                                                                                                   Mismatches 167;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                       HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A43507; A43507.
PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
109 INDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIERKKKNINTTPVDISIIDS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M18638; G153811; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFECT. IMMUN. 55:3228-3232(1987).

-!- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (REL. 17,
01-FEB-1991 (REL. 17,
15-JUL-1998 (REL. 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEHOE M.A., MILLER L., WALKER J.A., BOUINOIS G.J.; "Nucleotide sequence of the streptolysin O (SIO) gene: structural homologies between SIO and other membrane-damaging, thiol-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREPTOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 88057628.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACY_STRPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLASMID PMK157
                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 ARECTGLFWEWWRTVIDDRNLPLVKNRNVSIWGTTLYPRHSNNVDN 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               422 IDHSGGYVAQFNISWDEVSYDENGNEIKVHKKWGENYKSKLAHFTSSIYLPGNARNINIY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 QVYVKLSSSHSNKVKTAFEAAMSGKSVKGDVELTNIIKNSSFKAVIYGGSAKEEVEIID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 AXXDLLAKWHQDYGQVN-NVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 DGKVQEEVISFKQIYYNINVNEPTSPSKFFGGSVTKEQLDALGVNAENPPAYISSVAYGR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTIC CELL MEMBRANES.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNLGELRDILKKGSTYDRENPGYPISYTTNFLKDNDLAYVKNNSEYIETTSKSYTDGKIN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVT 304
                                                                             186;
                                                                                                                                                                                                                                                                                                             HEMOLYSIS; CYTOLYSIS; SIGNAL; PLASMID.
                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                                                                                                                                                                   571 AA;
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                                                                                                44.18;
                                                                                                                                                                                                63638 MW;
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LAST ANNOTATION UPDATE)
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                                                                   100; Mismatches 170;
                                                                                                Score 1379; DB 1;
Pred. No. 8.80e-269;
                                                                                                                                                                                                             BINDING TO CHOLESTEROL (BY SIMILARITY).
                                                                                                                                                                                                                                                       STREPTOLYSIN O.
                                                                                                                                                                                       33124E54 CRC32;
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                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OKUMURA K., HARA A., TANAKA T., NICHIGUCHI I., MINAMIDE W., IGARASHI H., YUTSUDO T.; "Cloning and sequencing the streptolysin O genes of group C and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
STREPTOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACY_STREQ
Q54114;
                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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      TOXIN; HEMOLYSIS; CYTOLYSIS; SIGNAL 1 36 CHAIN 37 574
                                                                                                PROSITE; PS00481; THIOL_CYTOLYSINS; PFAM; PF01289; Thiol_cytolysin; 1. HSSP; P19995; 1PFO.
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                                                                                                                                                                                                 EMBL; D16824; G498301; -
                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     streptococci.";
NA SEQ. 4:325-328(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTIC CELL MEMBRANES.
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                                      SIGNAL.
BY SIMILARITY.
             STREPTOLYSIN O.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACY_STRCB
Q53957;
              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 INDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIERKKKNINTTPVDISIIDS
                                                                                                                                                                                                                                                                                                    G streptococci.
                                                                                                                                                                                                                                                                                                                                        OKUMURA K., HARA A., TANAKA T., NICHIGUCHI I., MINAMIDE W., IGARASHI H., YUTSUDO T.;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 95102113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREPTOCOCCUS CANIS. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREPTOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
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                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                               "Cloning and sequencing the streptolysin O genes of group C and group
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREPTOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531 RECTGLAWEWWRKVIDERDVKLSKEINVNISGSTLSP 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 DHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI 425
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                                                                                                                                                                                              SEQ. 4:325-328(1994).
FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.
                                                                                                                                                                                 SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFVKLETSSKSNDVEAAFSAALKGTDVKTNGKYSDILENSSFTAVVLGGDAAEHNKVVTK 410
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Similarity 40.5%;
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574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 102; Mismatches 169;
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63991 MW;
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Pred. No. 5.24e-269;
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Best Local (
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                                                                                SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES (BY SIMILARITY).

-!- FUNCTION: HEMOLYTIC ACTIVITY AGAINST RED BLOOD CELL.

-!- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                  This SHIFE-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                         Q45105;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOXIN; HEMOLYSIS; CYTOLYSIS; SIGNAL.

SIGNAL 1 36 BY SIMILARITY.

CHAIN 37 574 STREETOLYSIN O.

ACT_SITE 533 533 BINDING TO CHOLESTEROL (BY SIMILARITY).
                                                                                                                                                                                                                                STRAIN-RIMD 206001;
                                                                                                                                                                                                                                                                                                                     BACILLUS CEREUS
                                                                                                                                                                                                                                                                                                                                    HEMOLYSIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
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PROSITE; PS00481; THIOL_CYTOLYSINS;
PFAM: PF01289; Thiol_cytolysin; 1.
HSSP; P1995; 1PFO.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                            TACY_BACCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHQGAYVAQYEILWDEINYDDKGKEVITKRRWDNNWYSKTSPFSTVIPLGANSRNIRIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYXRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEKKYMIAAYKQIFYTVSANLPNNPADVFDKSVTFKELQAKGVSNEAPPLFVSNVAYGRT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDNLVNQWHDNYSGGNTLPARTQYTESMYYSKSQIEAALNVNSKILDGTLGIDFKSISK 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIXVXAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.6%;
1 Similarity 40.3%;
184; Conservet'
                                                                                                                                                                                                                                                                                                     FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37
533
574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 100;
                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63910 MW;
institutions as long as its content
                                                                                                                                                                                                                                                                                                 BACILLUS/CLOSTRIDIUM GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1363; DB 1;
Pred. No. 3.49e-265;
100; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                  01-MAY-1991
01-MAY-1991
15-DEC-1998
                                                                                                                                                                                                                                                            AOFA_BOVIN P21398;
            MEDLINE; 89246344.

POWELL J.F., HSU Y.P.P., WEYLER W., CHEN S., SALACH J., ANDRIKOPOULOS K., MALLET J., BREAKEFIELD X.O.;

"The primary structure of bovine monoamine oxidase type with peptide sequences of bovine monoamine oxidase type flavoenzymes.";
                                                                                                                       BOS TAURUS (BOVINE).
EUKARYOTA; METAGOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00481; THIOL_CYTOLYS PFAM; PF01289; Thiol_cytolysin; HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      AMINE OXIDASE
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                            MAOA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOXIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D21270; G600252; -
                                                                                                                                                                                     (MAO-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                     425 IRECTGLAWEWWRTV 439
                                                                                                                                                                                                                                                                                                                                                                463 ARECTGLAWEWWRTI 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 SVANRTYPGAVQLANKAFADNQPSLLVAKRKPLNISIDLPGMRKENT-ITVQNPTYGNVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 SIDTGIGNLTYNNQEVLAVNGDKVESFVPKESINSNGKFVVVDVRKNHLQRHQSIFRLLD 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYYR
                                                                                                                                                                                                                                                                                                                                                                                           LDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDFNEIRNIIKDNAELSFKNPAYPISYTSTFLKDNATAAVHNNTDYIETTTTEYSSAKMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVYVKLETTSKSKDVQAAFKALLKNNSVETSGQYKDIFEESTFTAVVLGGDAKEHNKVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGEKKYMVAAYKQIFYTVSAELPNNPSDLFDNSVTFGELTRKGVSNSAPPVMVSNVAYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAVDDLVSTWNEKYSATHTLPARMQYTESMYYSKAQIASALNVNAKYLDNSLNIDFNAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TXDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNSSVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 41.5%;
Similarity 38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485 AA;
                                                                                                                                                                                                 (REL. 18, CREATED)
(REL. 18, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANOTATION UPDATE)
SE [FLAVIN-CONTAINING] A (EC 1.4.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466
485
259:407-413(1989)
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                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 POTENTIAL.
>485 HEWOLYSIN.
466 BINDING TO CHOLES:
485
485
485 AV; 45208ABA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIOL_CYTOLYSINS;
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Pred. No. 1
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING TO CHOLESTEROL
                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 154;
                                                                                                                                                                                                                                                                           527
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.40e-250;
                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                 .4) (MONOAMINE OXIDASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                               BOVINAE;
                           A. Comparison
B and other
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                                                                                                                               BOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.6%;
Best Local Similarity 18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                     01-JUL-1989 (REL. 11, CREATED)
01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                "MAS1, a gene essential for yeast mitochondrial assembly, subunit of the mitochondrial processing protease."; EMBO J. 7:1439-1447(1988).
                                                                                                                                                                                                                                                                                                                        P10507;
01-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X15609; G524; -.
EMBL; X15609; G525; ALT_INIT.
                                                                                                                                                                                    EUKARYOTA; FUNGI; ASCOMYCOTA; SACCHAROMYCETACEAE; SACCHAROMY
                                                                                                                                                                                                                                    (EC 3.4.24.64) (BETA-MPP) (PEP).
MAS1 OR MIF1 OR YLR163C OR L9632.10
                                                                                                                                                                                                                                                                                                                                                             MPPB_
STRAIN=S288C / AB972;
JOHNSTON M., ANDREWS S.,
                                 SEQUENCE FROM N.A.
                                                                                                                   WITTE C.
                                                                                                                                       MEDLINE; 88312592
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                      SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                            369 GAYVAQYYITWXELSYDHQGKEVLTPKAWD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310
                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 IAYL-DYNNLWRTM--DNMGKEIPADAPWE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 LETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGARVVTGKVDM 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 V-DYVDVGGAYVGPTQNRILRLSKQLGLETYKVNVNERLVHYVKGKTYPFRGAFPPVWNP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MESLQKTSDAGQMFDVVVIGGGISGISAAK-LLAEHEVNVLVLEARERVGGRTYTVRNEH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H(2)O(2).
COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: MONOMER, HOMO- OR HETERODIMER (CONTAINING TWO SUBUNITS SIMILAR SIZE). EACH SUBUNIT CONTAINS A COVALENTLY BOUND FLAVIN. ENZYMATICALLY ACTIVE AS MONOMER (BY SIMILARITY). SUBCELLULAR LOCATION: MITOCHONDRIAL OUTER MEMBRANE. SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CATALYZES THE OXIDATIVE DEAMINATION OF BIOGENIC AND XENOBIOTIC AMINES AND HAS IMPORTANT FUNCTIONS IN THE METABOLISM NEUROACTIVE AND VASOACTIVE AMINES IN THE CENTRAL MERVOUS SYSTEM AND PERIPHERAL TISSUES. MAO-A PREFERENTIALLY OXIDIZES BIOGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPINEPHRINE. CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMINES SUCH AS 5-HYDROXYTRYPTAMINE (5-HT), NOREPINEPHRINE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                           YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S03974; S03974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEDLIQEGSRFTADHPGLPISYTTSF-LRDNVVATFQNSTDYVETKVTAYRNGDLLLDHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                   ., JENSEN R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498
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                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLAVOPROTEIN; FAD; TRANSMEMBRANE; MITOCHONDRION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              406
518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59800 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                      SACCHAROMYCES
                                                                                                                  YAFFE M.P.,
 BRINKMAN R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 112; DB 1;
Pred. No. 6.96e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAD (ADP PART) (POTENTIAL).
FAD (BY SIMILARITY).
POTENTIAL.
; 724E4396 CRC32;
                                                                                                                                                                                                    HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 74; Indels
                                                                                                                   SCHATZ G.;
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 COOPER J.,
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SLAP_BACST P35825; 01-JUN-1994 01-JUN-1994

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ACT_SITE
METAL
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J. BIOL. CHEM. 266:6416-6423(1991).

-!- FUNCTION: THE MITOCHONDRIAL PROCESSING PROTEASE CLEAVES
-!- PRESEQUENCES FROM MITOCHONDRIAL PROTEIN PRECURSORS.
-!- CATALYTIC ACTIVITY: RELEASE OF N-TERMINAL TRANSIT PEPTIDES FROM PRECURSOR PROTEINS IMPORTED INTO THE MITOCHONDRION, TYPICALLY WIARG IN POSITION P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J.,
KUCABA T., HALLSWORTH K., HAWKINS J., HILLIER L., JIER M.,
JOHNSON D., LANGSTON Y., LARREILLE P., LE T.,
JOHNSON D., MENEZES S., MILLER N., NHAN M., PAULEY A., PELUS,
MARDIS E., MENEZES S., MILLER N., NHAN M., PAULEY A., PELUS,
RIFKEN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D.,
WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage hy and the EMBL outstat.

Institute. There are no restrictions on modified and this statement is not removed. Usage hy and an arrangement is not removed.
                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S00552; S00552.
PIR; A38734; A38734.
SGD; L0001026; MAS1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YANG M., GELI V., OPPLIGER W., SUDA K., JAMES P., SCHATZ G., "The MAS-encoded processing protease of yeast mitochondria. Interaction of the purified enzyme with signal peptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 21-32.
MEDLINE; 91177897.
                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                      TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROLASE; METALLOPROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00675; Insulinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00143; INSULINASE; 1.
                                                                                                                                           151
 265 ALIKGVKVAPQTEWKQ-ILDNTXVKAVILGG
                                  182 GPIKNIKSITRTDLKDYITKNYKGDRMVLAG
                                                                    210 PGDVFQDTVTVEDLKQRGISAERPLVYI-SX-VA--YXRQVYLKL-ETTSXSXEVEAAFE 264
                                                                                                       122 AVDILSDILTKSVLDNSAIERERDVIIRESEEVDKMYDEVVFDHLHEITYKDQPLGRTIL 181
                                                                                                                                                                        65 NNGTAHFLEHLAFK-GTQ-NRSQQGIELEIENI-GSHLNAYTSRENTVYYAKSLQEDIPK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY. SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INSULINASE FAMILY.
                                                                                                                                         EKXTAHSMEQLKVKFGSDFEKXGNSLDIDFNSVHSGEKXIQIVNXKQIYYTVSV-DAVKN 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U51921; G1234852; -.
                                                                                                                                                                                                              Similarity 33; Conser
                                                                                                                                                                                                                                                                                 462 AA;
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73
74
150
                                                                                                                                                                                                            Conservative
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462
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73
74
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ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                              Pred. 45; 1
                                                                                                                                                                                                                                                Score 108;
                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC; MITOCHONDRION; TRANSIT PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                      BETA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRIAL PROCESSING PROTEASE
                                                                                                                                                                                                                                                                                  438D1777
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                          No.
                                     212
   294
                                                                                                                                                                                                                            3; DB 1;
2.34e-01;
                                                                                                                                                                                                                                                                                  CRC32;
                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                              Length 462;
                                                                                                                                                                                                               Indels
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Best Local :
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                                                                                                                                                                                                          Q02008;
Q1-UUL-1993 (REL. 26, CREATED)
Q1-UUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
Q1-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3,4-DIHYDROXY-2-BUTANONE
THE C.Y., MEIGHEN E.A.;

The lux genes in Photobacterium leiognathi are closely linked genes corresponding in sequence to riboflavin synthesis genes."

BIOCHEM. BIOCHEY. RES. COMMUN. 186:690-697(1992).

-i- CATALYTIC ACTIVITY: GTP + 3 H(2)0 = FORMATE + 2,5-DIAMINO-(
                                                                                                                  STRAIN-ATCC 25521;
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                               PHOTOBACTERIUM
                                                                                                  MEDLINE; 92360014.
                                                                                                                                                                                        PHOTOBACTERIUM LEIOGNATHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL; CELL WALL; S-LAYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S34365; S34365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SURface-layer protein of Bacillus stearothermophilus strain PV72."; GENE 145:115-120(1994).

-!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                      318 S-RETADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG 361
                                                                                                                                                                                                                                                                                                                                                                                                   314 NIPFALNTADVSLSTDGKTITVDASTPFENNTEYKVVVKGIKDKNG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KUEN B., SLEYTR U.B., LUBITZ W.; "Sequence analysis of the sbsA gene encoding the 130-kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
S-LAYER PROTEIN PRECURSOR (SURFACE LAYER PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYXRQVYLKLETTSXSXEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 YDITV-AMKAR-EV-QDAVKAGNLDKAKAAVDQINQYLPKVTDAFKTELT-EVAKKALDA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACILLUS STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-PV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 23.5%; les 39; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF PROTEINS WHICH COAT THE SUBCELLULAR LOCATION: CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                -EAAFEALIKGVKVAPQTEWKQI-LDNTXVKAVILGGDPSSGARVVTGKVDMVEDLIQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEAALTPKVESVS-AINTQNKAVELTAVPVNGT-LKLQLSAAANEDTVNVNTVRIYKVDG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIA IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                    _PHOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X71092; G312730; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94320770
                                                                                                                                                                PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1228 AA;
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                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
43; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 108; DB 1;
Pred. No. 2.34e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-LAYER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                               364 AA
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                FORMATE + 2,5-DIAMINO-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1228;
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                                                genes.";
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                                                                                                 STRAIN-KIZ / MG1655;

STRAIN-KIZ / MG1655;

STRAIN-KIZ / MG16617.

BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND NELLEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F. GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
   KATO M.,
              \dot{x}-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS) OF 658-776 MEDLINE; 97207018.
                                                                  "The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                      IUCHI S., MATSUDA Z., FUJIWARA T., LIN E.C.C.; "The arcB gene of Escherichia coli encodes a sensor-regulator protein for anaerobic repression of the arc modulon."; MOL. MICROBIOL. 4:715-727(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1991 (REL. 19, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
AEROBIC RESPIRATION CONTROL SENSOR PROTEIN ARCB
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       MEDLINE; 90355832.
                                                                                                                                                                                                                                                                                                                                          STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         ESCHERICHIA COLI
                                                                                                                                                                                                                                                                                                                                                                                            ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P22763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARCB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PFAM; PF00925; GTP_cyclohydro2; 1.

PFAM; PF00926; DHBP_synthase; 1.

MULTIFUNCTIONAL ENZYME; RIBOFLAVIN BIOSYNTHESIS; HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROXY-4-(5-PHOSPHORIBOSYLAMINO)PYRIMIDINE + PYROPHOSPHATE.
-!- PATHWAY: RIBOFLAVIN BIOSYNTHESIS.
-!- SIMILARITY: TO OTHER BACTERIAL GTP CYCLOHYDROLASE II (RIBA), AND TO E.COLI RIBB AND V.HARVEYI LUXH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 -QILADLGVKKIRLLSNSNQGYRALSGFGLEVVE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 LAGLEPSSVIVEILNEDGSMARRPQLEIFAEKHGLKLGTIADLIEYRTQQESHIERISEY 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLKVKFGSDFEKXGNSLDIDFNSVHSGEKXIQIVNXKQIYYTVSV-DAVKNPGDVFQDTV 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELNTEYGI-FTLVTYRDTID-NQAHFALCKGEIQAKAATLVRVHVKDTLKDILQVGLSQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQILDNTXVKAVILGGDPSSGARVVTG-KVDMVE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVEDLKQRGISAERPLVYISXVAYXRQVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEW
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   MIZUNO T.,
                                                                                                                                                                                                                                                                                                                                                                                                   PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 AA; 39947 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
SHIMIZU T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 107; DB 1; Le
Pred. No. 3.15e-01;
57; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
HAKOSHIMA T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCE7130C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 11;
                                                                                                                                                 BURLAND V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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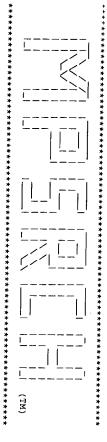
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                                                                                                                                                                                                                                                                                             Query Match 3.4%;
Best Local Similarity 18.6%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Insights into multistep phosphorelay from the crystal structure of the C-terminal HPt domain of ArcB."; CELL 88:717-723(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBMITTED (APR-1998) TO THE PDB DATA BANK.
-!- FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM ARCB/ARCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND A ASP OF THE RECEIVER DOMAIN (BY SIMILARITY).
-!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.57 ANGSTROMS) OF 657-774.
KATO M., MIZUNO T., SHIMIZU T., HAKOSHIMA T.;
                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
MOD_RES
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MODULON. ACTIVATES ARCA BY PHOSPHORYLATION.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECOGENE; EG10062; ARCB.
FRAM; PF00072; response_reg; 1.
FRAM; PF00512; signal; 1.
FRAM; PF00989; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X53315; G40951; -. EMBL; U18997; G606149; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: IN ITS C-TERMINUS, TO THE N-TERMINAL REGION OF THE REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1A0B; 18-MAR-98.
PDB; 2A0B; 17-JUN-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S11794; RGECAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000400; G1789603; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENSORY TRANSDUCTION;
                                                                                                                                                                                  304 LSRILLDTELTAEQEKYLKTIHVSAVT-LGNIFNDIIDMDKMERRKVQLDNQPVDFTSFL 362
                                                                                                                                                                                                                       124 RGAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDF-EKXGNSLDIDFNS 182
                                                                                                                                                                                                                                                          246 KVPYYDRVGKRHGLMGFGRDITERKRYQDALERASRD-KTTFISTISHELRTPLN-GIVG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RANSMEMBRANE;
                                                                                                                                             183 VHSGEKXIQIVNXKQIYY-TVSVDAVKNPGDVFQDTVTVEDLKQRGISAE-RPLVYISXV 240
 300 ARVVTGKVDMVEDLIQEGS 318
                                    421 VRVRYDEGDMLHFEVEDSG 439
                                                                                                          363 ADLENISALQAQQKGLRFNLEPTL-PLPHQV-ITDGTRLRQILMNLISNAVKFTQQGQVT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENSOR-REGULATOR PROTEIN FOR ANAEROBIC REPRESSION OF THE ARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBABLE)
                                                                         AYXRQVY-LKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSG 299
                                                                                                                                                                                                                                                                                                                                                                                              JUSTION: TRANSFERASE; KINASE; PHOSPHORYLATION;

1 1 22 CYTOPLASMIC (POTENTIAL).

23 50 POTENTIAL.

51 57 POTENTIAL.
58 77 POTENTIAL.
78 776 CYTOPLASMIC (POTENTIAL).
78 776 CYTOPLASMIC (POTENTIAL).
169 515 TRANSMITTER DOMATT.
16 776 RECEIVER POTENTIAL.
292 PHOOT
                                                                                                                                                                                                                                                                                                                                                                       468
776 AA;
                                                                                                                                                                                                                                                                                                                                                                           87824 MW;
                                                                                                                                                                                                                                                                                                                  Score 105; DB 1; Length 776; Pred. No. 5.67e-01;
                                                                                                                                                                                                                                                                                                   56; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
TRANSMITTER DOMAIN (POTENTIAL).
RECEIVER DOMAIN (POTENTIAL).
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
G -> GTG (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                           45AB596D CRC32;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3D-STRUCTURE.
                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                         9;
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Search completed: Mon Aug 30 16:10:58 1999 Job time : 46 secs.



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MPsrch_pp protein · protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 30 16:11:16 1999; MasPar time 28.94 Seconds 888.294 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score:

Sequence: >US-09-120-044-4
(1-471) from US09120044.pep
3127
1 MANKAVNDFILAMNYDXXKL.....TISIWGTTLXPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 49.293; Variance 92.130; scale 0.535

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

21111111 20087654321 2008754321	Result
1731 1732 1243 125 113 113 113 1113 1114 1114 1109 1009 1009 1009 1009 1009	Score
N N N N N N N N N N N N N N N N N N N	Query Match 1
50 50 50 50 50 265 265 745 745 745 746 746 710 1361 1361 1361 1361 146 1426 1426 1426 1426 1427 187 187	Length I
111112222222222222222222222222222222222	DB
055996 085102 031241 048773 042044 068518 067108 08708 087108 087108 087108 087109 088015 085906 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0685916 0675715 0675715 0675715	ID
SUILYSIN. HEMOLYSIN. PYOLYSIN. O (FRAGM LISTERIOLYSIN O (FRAGM LISTERIOLYSIN O (FRAGM LISTERIOLYSIN O (FRAGM CHROMOSOME XV READING CHROMOSOME XV READING HYPOTHETICAL 49.7 KD P DNA GYKASE A SUBUNIT. S-LAYER PROTEIN. S-LAYER PROTEIN. HYPOTHETICAL PROTEIN M GLUCOSE-6-PHOSPHATE IS TRANSPONSON PROTEIN B. HYPOTHETICAL 91.9 KD P FLAGELLAR HOOK ASSOCIA MUNIATIVE L-AMINO ACID MUNIATIVE L-AMINO ACID MUNIATIVE L-REGERIAN OF TRANSPONEDTICA KERATIN 14 (FRAGMENT). 1873A LONG HYPOTHETICA KERATIN 14 (FRAGMENT).	Description
0.00e+00 0.00e+00 2.24e-238 1.01e-03 7.12e-02 7.12e-02 7.10e-02 3.73e-02 3.73e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 1.79e-01 2.64e+00 3.52e+00 3.52e+00 3.52e+00 3.52e+00	Pred. No.

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OTEIN.	CTIN 200KD			SENSORY PROTEIN BVRS.	SIMILARITY TO C2H2-TYP	7-KETO-8-AMINOPELARGON		HYPOTHETICAL PROTEIN M	INE TRIPHOS	·	TEIN	<		CATION EFFLUX SYSTEM P	LATED PROTE	SIMILAR TO S. CEREVISI		TRANSDUCER-LIKE PROTEI	CONSERVED HYPOTHETICAL	FISSION YEAST.	ABC TRANSPORTER, ATP-B	AMINOTRANSFERASE.	HYPOTHETICAL PROTEIN M	PROLACTIN RECEPTOR (FR
6.22e+00		•	•	•	•		4.69e+00		•	•	•		U		ഗ	5	Մ			. 9	5		2.64e+00	

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241 AYXRQYYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGA 300	269 SYGRSMFIKLETSSRSTQVQAAFKAAIKGVDISGNAEYQDILKNTSFSAYIFGGDAGSAA 328	181 NSVHSGEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXV 240	209 DAVNSGEKQVQIVNEKQIYYTVSVDEPESPSKLFAEGTTVEDLKRNGITDEVPPVYVSSV 268	122 SVRGAXXDLLAKWHQDY-GQVNNVPARXQYEKXTAHSNEQLKVKFGSDFEKXGNSLDIDF 180	149 TVRTGVNNLLSKWNNTYAGEYGNTQAELQYDETMAYSMSQLKTKFGTSFEKIAVPLDINF 208	62 VXATXDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNS 121	89 VIDAKAANIYPGALLRADQNLLDNNPTLISIARGDLTLSLNLPGLANGDSHTVVNSPTRS 148	2 ANKAVNDFILAMNYDXXKLLTHQGESIENRFXKEGNQLPXEFVXXERKKRSLSTNTSDIX 61	29 SKQDINQYFQSLTYEPQEILTNEGEYIDNPPATTGMLENGRFVVLRREKKNITNNSADIA 88	Query Match 55.4%; Score 1731; DB 2; Length 497; Best Local Similarity 48.5%; Pred. No. 0.00e+00; Matches 227; Conservative 105; Mismatches 134; Indels 2; Gaps 2;		07; E1334304;	TTED	chara	SEGERS R.P.A.M., KENTER T., DE HAAN W.A.M., JACOBS A.A.C.;	1/7;	SEQUENCE OF 1-71 FROM N A		BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE:	DECOCOR SIL	SULV SULLYSIN.	999 (TREMBLREL.	EMBIREL OF CREATED)	?	SULT 1 Q55996 PRELIMINARY; PRT; 497 AA.	

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Matches 22
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O31241;
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01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Streptococcus suis type 2 hemolysin (suilysin) gene."; SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL, AF043556; G3309561; -. SEQUENCE 497 AA; 54778 MW; 36DAB184 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=1933;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GDLLLDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SALTLDHSGAYVAKYNITWEEVSYNEAGEEVWEPKAWDKNGVNLTSHWSETIQIPGNARN 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAVNSGEKQVQIVNFKQIYYTVSVDEPESPSKLFAEGTTVEDLKRNGITDEVPPVYVSSV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVRGAXXDLLAKWHQDY-GQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VXATXDSRLYPGALLVVDETXLENNPTLLAVDRAPMTYSXXLPGLASSDSFLQVEDPSNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKQDINQYFQSLTYGPQEILTNEGEYIDNPPATTGMLENGRFVVLRREKKNITNNSADIA 88
                                                                                                                                                                                LHVNIQECTGLAWEWWRTVYDK-DLPLVGQRKITIWGTTLYPQYADEV 495
                                                                                                                                                                                                                                                                    GDLLLDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRN 420
                                                                                                                                                                                                                                                                                                                                                                                         RVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRN 360
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                                                                                                                                                    LSVKIRECTGLAWEWWRTVYEKTDLXLVRKRTISIWGTTLYPQVEDKV
                                                                                                                                                                                                                                                                                                                           SALTLDHSGAYVAKYNITWEEVSYNEAGEEVWEPKAWDKNGVNLTSHWSETIQIPGNARN 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AYXRQVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKAVILGGDPSSGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
227; Conser
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                                  PRELIMINARY;
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48.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.00e+00;
104; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1726; DB 2; Pred. No. 0.00e+00;
                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497
                                  534
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Best Local (
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                                                                                                                                    Q48772
Q48772;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BILLINGTON S.J. JOST B.H., CUEVAS W.A., BRIGHT K.R., SONGER J.G.;
"The Arcanobacterium (Actinomyces) pyogenes hemolysin, pyolysin, is
novel member of the thiol-activated cytolysin family.";
J. BACTERIOL. 179:6100-6106(1997).
EMBL; U84782; 62252800; -.
PFAM; PF01289; Thiol_cytolysin; 1.
SEQUENCE 534 AA; 57873 MW; B0C14CA8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARCANOBACTERIUM PYOGENES.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; ACTINOMYCINEAE; ACTINOMYCETACEAE; ARCANOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TREMBLREL. 01-JAN-1998 (TREMBLREL.
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          SEQUENCE FROM N.A. STRAIN=11984, TYPE MEDLINE; 96118685.
RASMUSSEN O.F.,
                                                                                             LISTERIA MONOCYTOGENES
                                                                                                                       LISTERIOLYSIN O (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                            302
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                                                                   LISTERIA
                                                                                                                                                                                                                                                358
                                                                                                                                                                                                                                                                                                                                                                                     362
                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                         482 ARNIHVEAGEATGLAWDPWW-TVINKKNLPLVPHREIVLKGTTLNPWVEDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y Match
Local Similarity 38.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ETGVDKYIRGLKYDPSGVLAVKGESIENVPVTK-DQLKDGTYTVFKHERKSFNNLRSDIS
                                                                                                                                                                                                                                                                                                                                                                                  GGVEVATGNIDALKKIIKEESTYSTKVPAVPVSYAVNFLKDNQLAAVRSSGDYIETTATT 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVHSGEKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFDANNAHVYPGALVLANKDLAKGSPTSIGIARAPQTVSVDLPGLVDGKNKVVINNPTKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIHKRERQVAIASFKQIYYTASVDTPTSPHSVFGPNVTAQDLKDRGVNNKNPLGYISSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVRGAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSMEQLKVKFGSDFEKXGNSLDIDFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVTQGLNGLLDGWIQRNSKYPDHAAKISYDETMVTSKRQLEAKLGLGFEKVSAKLNVDFD
                                                                                                                                                                                                                                                                                                                                                           SGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTA
                                                                                                                                                                                                                                                                                                      YRNGDLLLDHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGN
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                                                                                FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
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                                                                                                                                     (TREMBLREL.
                                                                                                                                                                 (TREMBLREL.
                                                                                                                                                                                            PRELIMINARY;
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SKOUBOE P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05,
                                                                                                                                    01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 1243; DB 2; 1; Pred. No. 2.24e-238; 118; Mismatches 166;
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LAST ANNOTATION UPDATE)
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                                                                                                                                       LAST SEQUENCE UP
 DONS L.,
                                                                                                                                                                                             PRT;
                                                                                                                                                     SEQUENCE UPDATE)
  ROSSEN L.,
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  OLSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
  J.E.;
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RESULT IN ACCORDANCE OF THE PROPERTY OF THE PR
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Best Local
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01-NOV-1996
01-NOV-1996
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q12044 PRELIMINARY; PRT; 265 AA.
Q12044;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
CHROMOSOME XV READING FRAME ORF YOR220W.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                         THIERRY A., DUJON B.; SUBMITTED (JUL-1996)
                                                                                                                                                                                                                         SEQUENCE FROM N.A.

BOYER J., FAIRHEAD C., GAILLON L., GALISSON F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               evidence from flagellin, invasive associated listeriolysin O genes."; MICROBIOLOGY 141:2053-2061(1995).
                                                                                                                                                                                                                                                                                                                                                      SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-206.1.1, TY
                                 SUBMITTED (JUL-1996) TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 96118685
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MICROBIOLOGY 141:2053-2061(1995).
                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 4.0%;
Local Similarity 34.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 3.8%;
Local Similarity 34.7%;
les 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NSSFKAVIYGGFAKDEVQIIDGNLGDLRDILKKGATFNRETPGVPIAYT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X85935; G940637; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TREMBLREL. 01, CREATED)
(TREMBLREL. 01, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE 2A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5368 MW;
                                                                                                                                                                             ТО
                             EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                  EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 119; DB 2;
Pred. No. 7.42e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A4B59721 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 125; DB 2;
Pred. No. 1.01e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 50;
                                                                                                                                                                     BANKS
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                                                                                                                                                                                                                                        MICHAUX
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Best Local
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Best Local (
                                                                                                                     067108;
067108;
01-AUG-1998
01-AUG-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE: 96347136.
MEDLINE: 96347136.
TRUDEAU K.G., WARD M.J., ZUSMAN D.R.;
"Identification and characterization of FrzZ, a novel response "Identification and characterization of FrzZ, a novel response regulator necessary for swarming and fruiting-body formation if regulator manthus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O68518 PRELIMINARY; PRT; 450 AA.
O68518; O1-AUG-1998 (TREMBLREL. 07, CREATED)
O1-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYPOTHETICAL 49.7 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBMITTED (OCT 1995) TO EMBL/GE
EMBL; 275128; E252085; -
EMBL; 275141; G1050772; -
EMBL; X92441; G1050772; -
265 AA; 29255 MW;
                                                                                                  DNA
                                                                          GYRA.
                     BACTERIA; AQUIFICALES;
                                               AQUIFEX AEOLICUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WARD M.J., ZUSMAN D.R.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AF049107; G2947295; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA; PROTEOBACTERIA; DELTA SUBDIVISION; MYXOBACTERIA; MYXOCOCCALES; CYSTOBACTERINEAE; MYXOCOCCACEAE; MYXOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYXOCOCCUS XANTHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    233
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                                                                                                                                                                                                                                                                                                                               291
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                                                                                                                                                                                                                                                                                                                                                                  66 HLPGRLPVGLHPETGELELVREMKVGGKTFVPNAVGALLPPGYTRTFLPGEV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 FVXXERKKRSLSTNTSDIXVXATXDSRLY-PGALLVVDETXLENNPTL-LAVDRAPMTYS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 PLVLVTSDMTFAPKL-LFADPKGRVMEHPYLLATLRSGEELVPPQD-KPIPLPSTG-RLV 65
                                                                                               GYRASE A SUBUNIT
                                                                                                                                                                                                                                                                                                                       ILGGDPSSGARVVTGKVDMVEDLIQEGSRFTADHPG--LPISYTTSFLRDNV
                                                                                                                                                                                                                                                                                                                                                                                                                       PLVYI-SXVAYXRQVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQI-LDNTXVKAV
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Similarity 35.2%;
25; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%;
Similarity 26.8%;
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                                                                                                                     (TREMBLREL.
(TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450 AA;
                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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               AQUIFICACEAE; AQUIFEX
                                                                                                               07, CREATED)
07, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 113; DB 2;
Pred. No. 5.12e-02;
25; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 113; DB 3; Le Pred. No. 5.12e-02; 10; Mismatches 33;
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E3A6FC67 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                       744
                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L. GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBEI FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-LAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The S-layer protein from Campylobacter rectus: sequence determination and function of the recombinant protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-ATCC 33238; MEDLINE; 98442421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMPYLOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-LAYER PROTEIN.
CAMPYLOBACTER RECTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     087083;
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STRAIN=VF5;
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353
                                                           231
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                                                                                                                                                                                                                                                                                                                                                                                                        3.6%;
Local Similarity 19.9%;
CS 37; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSIIPVEELPLEKAP-VVNILRVPFTEGLFL
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LSITSD 358
                                                                                                                                                                                                                                                                                                 VEDPSNSSVRGAXXDLLAKWHQDYGQVNNVPARXQYEKXTAHSME-QLKVKFGSDFEKXG 173
                                                                                                                                                                                                                                                                                                                                                            VDWHSNPEHPGKAYELTTNTDNATANVFNAPMK-HNPGGTDRIMTLQSSDKLTGDYSRHD 236
                                                           ERPLVY - ISXVAYXRQVYLKLETTSXSXEVEAAFEALIKGVKVAPQTEWKQILDNTXVKA
                                                                                                                    EAGNKFNVESIG-QKLVGMRLANVAK-KDIDVKFEH-KKGVLSGFEDKSNVFLENVEAKS 352
                                                                                                                                                                            NSLDIDFNSVHS--GEKXIQIVNXKQI-YYTVSVDAVKNPGDVFQDTVTVEDLKQRGISA
                                                                                                                                                                                                                                        NTLNVEFGQANADEGDPTSRTPTLTNIQNINIEVTGTVNTLDL-RDSNDVEKINIHRITK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98196666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1361 AA;
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larity 24.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144904 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KITANAKA M., KOKEGUCHI S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPSILON SUBDIVISION; CAMPYLOBACTER GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 114; DB 2; Length 1361; Pred. No. 3.73e-02; 50; Mismatches 89; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 10;
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HUBER
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Best Local
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01-JAN-1998
01-JAN-1998
01-NOV-1998
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Q58691
Q58691;
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"A new member of the S-layer protein family: characterization crs gene from Campylobacter rectus.";
INFECT. IMMUN. 66:1521-1526(1998).
                                                     SEQUENCE FROM N.A.

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

KERLANAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

OVERBEEK R., KIXKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii",

SCIENCE 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TREMBLREL. 06, 01-JUN-1998 (TREMBLREL. 06, 01-JUN-1998 (TREMBLREL. 06, HYPOTHETICAL PROTEIN MJ1295.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARCHAEA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHANOCOCCUS JANNASCHII.
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      M.THERMOAUTOTROPHICUM MTH576
                               SIMILARITY: STRONG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6%;
Similarity 19.9%;
37; Conservation
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(TREMBLREL. 05,
(TREMBLREL. 08,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHANOCOCCALES; METHANOCOCCACEAE;
                               TO A. FULGIDUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPSILON SUBDIVISION; CAMPYLOBACTER GROUP;
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LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                   KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
MOL. MICROBIOL. 21:77-96(1996).
EMBL; AL031107; E1311951;
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A3(2);
PARKHILL J., BARRELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2);
SEEGER K.J., HARRIS D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREPTOMYCES COELICOLOR.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TREMBLREL 08, 01-NOV-1998 (TREMBLREL 08, 01-NOV-1998 (TREMBLREL 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         088015;
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225 QRGISAERPLVYISXVAYXRQVYLKLETTSXSXEVEAAFEALI 267
                                                                                                                                                                                                                                                                                                                                                                                REDENBACH M.,
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED (JUL-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCOSE-6-PHOSPHATE ISOMERASE.
                                                             166
                                                                                                                                 305 EHFRNAEAPANAPL---LLGLLGVWYGDFLGAQSHAVLPYSHYLSKFTAY-LQQLDMESN 360
                                                                                                                                                                                       245 ALSTNAEKVADFGIDTANNFEFWDWVGGRYSFDSAIGLSLMIAIGPDRFREMLDGFRIVD 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U67570; G1591933; -. HYPOTHETICAL PROTEIN. SEQUENCE 218 AA; 24666 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230
                                                                                                                                                             52 SLSTNTSDIXVXATXDSRLYPGALLVVDETXLENNPTL-LAVDRAPMTYSXXLPGL-ASS 109
                                                                                                                                                                                                                                      Watch 3.5%;
Local Similarity 22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 KXGNSLDIDFNSVHSGEKXIQIVNXKQIYYTVSVDAVKNPGDV-FQDTVTVEDLKQRGIS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 VE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 KKAKDLGAEIVVVH-GETVVEPVEEKTNYYASISEDVDILAHPGFIDKETAENLKENDIF 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                           GKSVDREGNPVQWQTGPVVWG-TP-GT-NGQHAYYQLIHQGTKLIPADFIGFARPVDELS 417
                                                                                                        DSFLQVEDPSNSSVRGAXXDLLAKWHQDY-G-QVNNVPARXQY-EKXTAHSMEQLKVKF- 165
                           E-ELKAQHDLLMANFFA-QTQA-LAFGKTPDEVRAEGVPEELV 457
                                                  GSDFEKXGNSLDIDFNSVHSGEKXIQIVNXKQIYYTVSVDAVK-NPGDVFQDTVTVEDLK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE 231
                                                                                                                                                                                                                                                                                                                                                            97600351.
H M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n 3.5%;
Similarity 30.6%;
19; Conservative
                                                                                                                                                                                                                                                                                 550 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                60424 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24666 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                G., RAJANDREAM M.A.
EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                         Score 110; DB 2;
Pred. No. 1.31e-01;
53; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109; DB 1;
Pred. No. 1.79e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches 29; Indels
                                                                                                                                                                                                                                                                             028FD1F6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CFC99AB9 CRC32;
                                                                                                                                                                                                                      Mismatches 104; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               DATA BANKS
                                                                                                                                                                                                                                                   Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                                      Gaps 15;
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RESULT

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246 VYLKLETTSXSXEVEAAFEALIKG

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                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                          EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
EMBL; AL022250; E1287635; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

BEVAN M., VAN DER SCHUEREN J., CHUANG Y-J., VOET M., ROBBEN J.

VOLCKAERT G., BANCROFT I., MEWES H.W., MAYER K.F.X., SCHUELLER

VOLCKAERT (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MACMOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             065715
065715;
                                                                                                                                                                                                                                                                                 HYPOTHETICAL PROTEIN SEQUENCE 814 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TREMBLREL 07, CREATED)
01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T5K18.220
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01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAPPARALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK E.C., SENSEN C.W., GAASTERLAND T., SAFFER J.D., FREDRICKSON J.K.; "Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromaticivorans strain F199."; SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 085906;
                                                                187
                                                                                                                    729
788 GGV-LEAFKGSDE-EN-YAAIIEG 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLASMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; ZYMOMONAS GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLASMID
                                                                                                                                                          3.5%;
Local Similarity 25.0%;
es 21; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 3.5%;
Local Similarity 22.6%;
les 14; Conservative
                                              EKXIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXV-AYXRQ 245
                                                                                                EMHSKNVHPNKITYTVMIGGYARDGNVTEASRLLNEMREKGIVPD-SITYKEFIYGYLKQ 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DHSGAYVAQYYITWXELSYDHQGKEVLTPKAWDRNGQDLTAHFTTS-IPLKGNVRNLSVK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ていた
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BRASSICACEAE; ARABIDOPSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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(TREMBLREL.
(TREMBLREL.
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                                                                                                                                                                                                                                                                            91943 MW; A41B8987 CRC32;
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                          Score 108; DB 10; 1
Pred. No. 2.43e-01;
26; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 109; DB 2; Le
Pred. No. 1.79e-01;
20; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41B48670 CRC32;
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                                                                                                                                                                                                                 Length 814;
                                                                                                                                                             Indels
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                                                                                                                            Query Match 3.4%;
Best Local Similarity 23.7%;
Matches 22; Conservative
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067578 PRELIMINARY; PRT; 426 AA.
067578: 01-AUG-1998 (TREMBLREL 07, CREATED)
01-AUG-1998 (TREMBLREL 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
FLAGELLAR HOOK ASSOCIATED PROTEIN FLCK.
                                                                                                                                                                                          FLAGELLA.
SEQUENCE
                                                                                                                                                                                                                     DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AE000749; G2983977; -.
                                                                                                                                                                                                                                                                                                                                                                     MEDITIE; 98196666.

DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;

"The complete genome of the hyperthermophilic bacterium Aquifex acclicus.";
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                                                  aeolicus.";
NATURE 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQUIFEX AEOLICUS.
BACTERIA; AQUIFICACEAE; AQUIFEX.
221 EDLKQRGISAERPLVYISXVAYXRQVYL-KLET 252
                                                          164 KFGSDFEKXGNSLDIDFNSVHSGEKXIQIVNXKQIYYTVSVDAVK-N--PGDVFQDTVTV 220
                              59 QNENFINTRNEK-LSYVSYLE-ERRDYLSKLES 89
                                                                                426 AA; 49567 MW; 47417AE0 CRC32;
                                                                                                                          Score 106; DB 2; Length 426; 
Pred. No. 4.47e-01; 
24; Mismatches 39; Indels
                                                                                                                                 Gaps
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Search completed: Mon Aug 30 16:12:37 1999 Job time: 81 secs.

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3239 14063 114098 11398 11398 11398 11398 1114 1114 1114 1114 1108 1108 1108 110	de de		prote prote	**************************************
12444499 244433333334449 234433333333449	is the nater than rived by	a-geneseq3 1:part8 8:part8 14:part1 14:part1 24:part2 29:part2 29:part3 34:part3 39:part3	Distributi pin - protei Mon Aug 30 ot generated >US-09-120- (1-471) fro 3241 1 MANKAVNDF PAM 150 Gap 11 170751 seqs Minimum Mat Listing fir	3.12
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R05923 R05924 R33842 R33841 R10376 R6000 W60952 R88135 R77673 R272673 W227673 W55347 W55347 W5528 W60976 W5528 W60976 W5528	results to the to the to the summarin	35; Variance 169.5	summan	
Immunogenic pneumolys Immunogenic pneumolys Streptolysin O varian Soluble streptolysin Streptolysin O deriva Bacteriophage lambda Streptococcus pneumon Listeriolysin O haemo S-layer protein encod Bacillus stearothermo H. pylori ORF 01cell6 Streptococcus pneumon H. pylori ORF 02e9303 Monamine oxidase A. Human monoamine oxida	icted by chance to e of the result bei score distribution escription	4:part4 5:part5 6:part6 0 11:part11 12:part12 1 art16 17:part17 18:part art21 22:part22 23:part art45 27:part47 28:part art45 32:part32 33:part art46 37:part37 38:part art46 37:part37 38:part47	rd Molecular Ltd rd Molecular Ltd , using Smith-Waterm ssPar time 18.51 Sec 11.196 Million cell 12.29 dues Residues	nguting * * * * * * * * * * * * * * * * * * *
3.78e-273 1.96e-127 1.96e-110 7.62e-110 3.17e-109 2.31e-03 8.63e-20 6.06e+00 4.45e+00 4.45e+01 1.12e+01	have a ng printed,	5 7:part7 13:part13 12:8 12:23 12:28 13:33 13:38	ithm (27, 25, 27, 27, 27, 27, 27, 27, 27, 27, 27, 27	** ** ** ** ** ** ** ** ** ** ** ** **
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Score Pred. 1; 1; 1; 1; 1; 1; 1; 1; 1; 1; 1; 1; 1;	1 AA. nia; nia; IS G. IS G. IS G. IS G. IS G. IS G. Ish. ntigg	R07691 R41781 W306264 W306267 W471290 W471290 W472067 R72096 R72096 R72096 R72096 R840187 R966737 R966737 R966737 R966737 R967367 W119506
NO. 3 Mismat No. 3 Mismat IIIII IIIII IIIII IIIII IIIII IIIIIII IIII	meningit: , ANDREW , ANDREW procedus procedus anic to w. n against	w ·
DB 1 3,78e-2 ches ches	(EW PW, us pneumol us pne	Myobac: Rabbit Klebsi Glycar Potato Potato HSV-2 Gracil: Fungus Glucan HSV-2 HSV-2 HSV-2 HSV-1 Potato Plasmo Arabid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaccines are non-toxic and antigenic to wild type pneumolysin, making them useful in vaccination against pneumonia and associated meningitis, bacteriaemia etc.

Sequence 471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers misc_difference 428
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16-DEC-1988; AU-001989.
(PATO/) PATON J C.
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Pneumolysin; vaccine; pneumonia;
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Pred. No. 2.07e-257;
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The sequence represents a soluble variant of Streptolysin O (SLO) having no haemolytic activity. The variant SLO can specifically recognise wild-type anti-SLO antibodies (ASO) but has no haemolytic activity. It can be used for the determination of previous and/or current infection by Streptococcus pyogenes. It enables ASO assays to become commercially viable and avoids the risk of handling haemolytically active S. pyogenes wild-type SLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptolysin O variants produced by recombinant DNA technology having no haemolytic activity and recognised by wild-type anti-streptolysin O antibodies, useful in diagnosis of
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03-AUG-1992; U06380.
30-AUG-1991; US-752/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 43.9%;
Similarity 42.2%;
193; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-752428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity; wild type; anti-SLO antibodies;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.96e-111;
104; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1423; DB 6;
Pred. No. 1.96e-111
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wild-type Streptolysin O
Claim 7; Fig 2; 60pp; English.
The sequence is that of a soluble deriv. of Streptolysin O
with haemolytic properties which was obtd. from Streptococcus pyogenes
genomic library clone rSLO.3. It is useful in immunodiagnostic assays
which rely upon, e.g. the haemolytic properties of wild type
Streptolysin O. Recombinant Streptolysin O is obtd. more cheaply
than purified Streptolysin O obtd. from Streptococcus pyogenes.
                           437 sectglawewwrkviderdvklskeinvnisgstlsp 473
         426
                                                                                                                              306 KVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFONSTDYVETKVTAYRNGDLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deriv. of streptolysin 0 with haemolytic activity - used ir immuno-diagnostic assays which rely on haemolytic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams CW, Wang EY; WPI; 93-100980/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-1992;
30-AUG-1991;
                                                                                                                                                                                                                                                                                  186
                                                                                                                                                                                                                                                                                                                                     126 AVNDLLAKWHQDYGQVNNVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHS 185
                                                                                                                                                                                                                                                                                                                                                                   137 aidnlvngwhdnysggntlpartqytesmvysksqieaalnvnskildgtlgidfksisk 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
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                                                                                                                                                DHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI 425
                                                                                            shqqayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgansrnirima 436
                                                                                                                                                                                                 VILKLETTSKSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVTG
                                                                                                                                                                                                                       vfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaaehnkvvtk 316
                                                                                                                                                                                                                                                                  GEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQ 245
                                                                                                                                                                                                                                                                                                  gekkvmiaaykqifytvsanlpnnpadvfdksvtfkelqrkgvsneapplfvsnvaygrt 256
RECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                        NDSRLYPGALLYVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                     vtdrtypaalqlankgftenkpdavvtkrnpqkihidlpgmgdkat-vevndptyanvst 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNDFILAMNYDKKKLLTHQGESIENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVTAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rectglawewwrkviderdvklskeinvnisgstlsp 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.4%;
al Similarity 41.8%;
191; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.4%; Score 1405; DB 6; Length 48 .larity 41.8%; Pred. No. 7.62e-110; Conservative 104; Mismatches 161; Indels
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US-752429
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Best Local
                                   Bacteriophage lambda PL promoter - streptolysin O (SLO) fusion protein of plasmid pMK306. Streptolysin O; SLO; protease; bacteriophage lambda; ds.
          Streptococcus pyogenes.

Location/Qualifiers
                                                                                          R06000;
22-NOV-1990 (first entry)
                                                                                                                            R06000 standard; protein;
cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2: 9pp; English.

The SLO derivative contains no cysteine residues, with cytolytic activity giving resistance to inactivation by oxidation or thiol groups. Abs raised to the SLO may be used in the dection and diagnosis of Streptococcus pyogenes infection.
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                                                                                                                                                                                             426 RECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deriv. of thiol-activated protein streptolysin O - contg. no cysteine amino acid but retaining cytolytic activity, used for detecting antibodies in samples Disclosure; Fig 2; 9pp; English.
                                                                                                                                                                                                                             528 reatglawewwrkviderdvklskeinvnisgstlsp 564
                                                                                                                                                                                                                                                           366 DHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI 425
                                                                                                                                                                                                                                                                                         468 shqqayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgansrnirima 527
                                                                                                                                                                                                                                                                                                                               306 KVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLL
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N-PSDB; Q10320.
                                                                                                                                                                                                                                                                                                                                                                                                                            348 vfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaaehnkvvtk 407
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(PINK/) PINKNEY M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptolysin O derivative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 aidnlvngwhdnysggntlpartgytesmvysksgieaalnvnskildgtlgidfksisk 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 vtdrtypaalglankgftenkpdavvtkrnpgkihidlpgmgdkat-vevndptyanvst 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 indkiyslnynelevlakngetienfvpkegvkkadkfivierkkkninttpvdisiids 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 NDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 43.1%; Score 1398; DB 2; Local Similarity 41.8%; Pred. No. 3.17e-109; PS 191; Conservative 104: Winner 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 VNDFILAMNYDKKKLLTHQGESIENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVTAT 65
                                                                                                                                                                                                                                                                                                                                                           dfdvirnvikdnatfsrknpaypisytsvflknnklagvnnrteyvettsteytsgkinl 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gekkvmiaaykqifytvsanlpnnpadvfdksvtfkelqrkgvsneapplfvsnvaygrt 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVNDLLAKWHQDYGQVNNVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 104; Mismatches 161; Indels 1;
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                             Query Match
Best Local S
Matches 14
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18-MAY-1990.
17-NOV-1989; 026008.
18-NOV-1988; GB-027038.
17-NOV-1989; GB-026008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to streptolysin O.

Disclosure; pp; English.

SLO derivative is epitopic to its wild type parent, and may be used in detecting anti-SLO Abs, indicating presence of Strepton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-toxic and non-cytolytic derivs. of streptolysin O - used for raising antibodies, purifying antibodies or detecting antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; Q05240.
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of meningitis
Claim 11; Page 53; 130pp; English.
Claim 11; Page 53; 130pp; English.
The sequence is that of the polypeptide encoded by a region isolated from S. pneumoniae which shows homology to pneumolysin.
The protein, or agonists of it, may be useful as an antibacterial for The protein, or agonists of it, may be useful as an antibacterial for
                                                                                                                                                                                  27-OCT-1997; U19226.
01-NOV-1996; US-029930.
(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Black MT, Hodgson JE, Knowles DJ(
Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                           Streptococcus pneumoniae encoded polypeptide. coding region; ORF; open reading frame; antibacterial;
                                                                                                                                                                                                                                                                                                           WO9819689-A1.
                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 PSNSSVRGAVNDLLAKWHQDYGQVNNVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLD 177
                                                                                                                New isolated nucleic acids from Streptococcus e.g. for identifying anti-bacterial(s) for trees.
                                                                                                                                                  N-PSDB; V37352
                                                                                                                                                                                                                                                                                                                                                                                                                                  W60952 standard; Protein; 113 AA
                                                                                                                                                                                                                                                                                                                                                infection;
                                                                                                                                                                                                                                                                                                                                                                                               3-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    418 VRNLSVKIRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 srnirimarectglawewwrkviderdvklskeinvnisgstlsp 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 YRNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGN 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 ytsgkinlshqgayvaqyeilwdeinyddkgkevitkrrwdnnwysktspfstviplgan 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 34.1%;
Local Similarity 43.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aanpllvgvsakpvngwhdnyspgntlpartgytesmvysksqieaalnvnskildgtlg 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90-217310/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              snvaygrtvfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaa 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                idfksiskgekkvmiaaykqifytvsanlpnnpadvfdksvtfkelqrkgvsneapplfv 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ehnkvvtkdfdvirnvikdnatfsrknpaypisytsvflknnkiagvnnrteyvettste 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDFNSVHSGEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SXVAYGRQVYLKLETTSKSXEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPS 297
                                                                                                                                                                       98-286586/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371 AA;
                                                                                                                                                                                                                                                                                                                                            prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=Lambda N promoter – SLO.
                                                                                                                                                                                                          Knowles DJC, Lonetto MA, Nicholas
                                                                                                                                                                                                                                                                                                                                                meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1104; DB 1; Length 371; pred. No. 2.51e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 121; Indels
                                                                                                                     treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Streptococcus

    useful,
    prevention

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                                                                                                                                      useful,
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                                                   밁
                                                                                                                                                                                                                                          rinternalises polynucleotide (PN) into endosome, then lyses endosome of the release PN into cell's cytoplasm

Example 3; Page 13; 23pp; English.

C (HD) fragment, which is 100% conserved in the LLO homologues (HD) fragment, which is 100% conserved in the LLO homologues of the properties of the full length LLO coding sequence in a coluble molecular complex, for the specific targetting of a collynucleotide (PN) to a cell. The complex comprises a PN, a converted into a surface mol. of the cell and is carrier comprising a PN binding agent and a cell specific binding carrier comprising a PN binding agent and a cell specific binding contennalised into an endosome, and a bacterial component (i.e. the PN into cell's cytoplasm. The complex can be used therapeutically concentration call in vivo, ex vivo or in vitro delivery of a PN to a central component of a PN to 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.3%;
Best Local Similarity 43.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                         Query Match
Best Local 9
                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial gene expression. Detecting a sequence encoding the protein can be used diagnostically, e.g. to detect a mutation for serotyping or classifying infectious agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeriolysin 0; haemolytic; domain; streptolysin 0; pneumolysin; soluble molecular complex; specific; targetted; polynucleotide; endosome lysis; bacterial component; cytoplasm; therapeutic; in vivo; ex vivo; in vitro; delivery; cell specific; hemolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JAN-1996.
27-JUN-1995; U08091.
29-JUN-1994; US-267710.
07-JUN-1995; US-484009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R88135;
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R88135 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeriolysin O haemolytic domain peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soluble molecular complex for specific targetting of PN to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carmichael E, Sp. WPI; 96-077502/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9600792-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 RNLSVKIRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQV-EDKV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 RNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNV 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TARG-) TARGETECH INC. (UYCO-) UNIV CONNECTICUT.
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                               specific
427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 rnlrvkiekktgllwnrwqtiyenrpilaqphrkithwgttlnskvsdddv 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0%;
                                                   1 ectglawewwr 11
ECTGLAWEWWR 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TARGETECH
                                                                                                      11;
                                                                                                                                                                                                                                  ce1.
                                                                                                                                                                                                         11 AA;
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                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spitalny GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 367; DB 33;
Pred. No. 8.63e-20;
32; Mismatches 30
                                                                                                                              Score 112; DB 17;
Pred. No. 6.06e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu CH,
                                                                                                        0
                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specifically caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 113;
                                                                                                                                                         Length 11;
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                                              (LUBI/) LUBITZ W.
(SLEY) SLEYTR U.
Kuen B. Lubitz W.
WPI; 97-394558/37.
N-PSDB; T75487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus stearothermophilus S-layer protein sbs-A.
S-layer; sbs-A; vaccine; adjuvant; carrier; hybridisation assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   s-iayer; sbs-A; vaccine; adjuvant; carrier; molecular spinning nozzle; molecular laser.
                                                                                                                                                                                01-FEB-1996; 003649.
01-FEB-1996; DE-003649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W22862 standard; Protein; 1228 AA.
                                                                                                                                                                                                                                                                     DE19603649-A1.
                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 6-7; 12pp; German.

The claimed signal peptide encoding sequence (see tag e of T08695) is pref. operably linked at the 3' end to a protein encoding sequence. The protein is pref. the S-layer protein (see tag f of T08695). At the 5' end, the signal peptide encoding sequence is pref. linked to an expression control sequence, pref. the sequence given in T08696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 S-RFTADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 nipfalntadvslstdgktitvdastpfennteykvvvkgikdkng 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 -EAAFEALIKGVKVAPQTEWKQI-LDNTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding signal peptide of Bacillus stearothermophilus S-layer protein - which has a lysine content of at least 10 per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQVYLKLETTSKSXEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 yditv-amkar-ev-qdavkagnldkakaavdqingylpkvtdafktelt-evakkalda 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; T08695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VOGE-) VOGELBUSCH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-1994; 425527.
19-JUL-1994; DE-425527.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 24.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deaaltpkvesvs-aintqnkaveltavpvngt-lklqlsaaanedtvnvntvriykvdg 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96-077933/09.
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of S-layer proteins by expressing sbs-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1228 AA;
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                                                                                                                                                                                                                                                                                                                                       /label=_sig_peptide
                                                                                                                                                                                                                                                                                         /label= mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= mat_protein
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                                                                                               Sleytr U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by sbsA gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 114; DB 17;
Pred. No. 4.45e+00;
44; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1228;
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  gene in Gram
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PT Helicobacter pylori nucleic acid sequences and encoded prolypeptide(s) - useful in vaccines to treat or prevent H. pylori prolypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection

CC Claim 14; Page 571; 1145pp; English.

CC This sequence is a H. pylori protein of unspecified function.

CC This sequence is a H. pylori protein of prevent or treat H. pylori compounds, and probes derived from it may be used for the identification of the pylori in a sample and the diagnosis of H. pylori infection. Nucleic can be used to prevent the translation of H. pylori infection. Nucleic can be used to prevent the translation of H. pylori mRNA. Antibodies and against the protein can be used in immunoassays to evaluate the abundance can be used in the protein can be used in immunoassays to evaluate the abundance of by mechanically shearing the bacterial DNA. The sequences were analysed can defined by computer evaluation. To identify likely H. pylori antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erg School of the School of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or new sbs-B gene in any host, also new recombinant proteins containing heterologous inserts, e.g. of repitope(s), useful as vaccines and adjuvants

Claim 1: Pages 9-14; 31pp; German.

Crace The present sequence is the Bacillus stearothermophilus pv72

Claim 2: Payer protein, sbs-A. S-layer structures can be used as vaccines or adjuvants, particularly when they include a bacterial ghost that crecombinant sbs-A, depending on the nature of the inserted peptide, crecombinant sbs-A, depending on the nature of the inserted peptide, care as an universal carrier for biotinylated reactants for use in conduce immune responses (epitopes), as a reagent for removing contains and recombination assays (the insert is streptavidin), and the contains of the insert is streptaviding contains and carrier for series of the insert is streptavidin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 97-503122/46.
N-PSDB; V24756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9737044-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. Pylori ORF 01ce11618orf11 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W55347 standard; Protein; 188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ASTR ) ASTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 S-RFTADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spinning nozzle (polyhydroxybutyrate synthase) and as a molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine or toxin from serum (antigenic epitopes), as a molecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 nipfalntadvslstdgktitvdastpfennteykvvvkgikdkng 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 -EAAFEALIKGVKVAPQTEWKQI-LDNTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 deaaltpkvesvs-aintqnkaveltavpvngt-lklqlsaaanedtvnvntvriykvdg 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGRQVYLKLETTSKSXEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 yditv-amkar-ev-qdavkagnldkakaavdqinqylpkvtdafktelt-evakkalda 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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40; Conservative
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Pred. No. 4.45e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1228;
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                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                      PT of meningitis

PS Claim 1; Page 71-72; 130pp; English.

CC The sequence is that of the polypeptide encoded by a region isolated CC The sequence is that of the polypeptide encoded by a region isolated CC The sequence is that of the polypeptide encoded by a region isolated CC phosphorylase. It, or agonists of it, may be useful as an anti-

CC phosphorylase. It, or agonists of it, may be useful as an anti-

CC phosphorylase. It, or agonists of it, may be useful as an anti-

CC phosphorylase. It, or agonists of it, may be useful as an anti-

CC phosphorylase. It, or agonists of infection, specifically caused by 5, pneumoniae (particularly meningitis) but possibly also Helicobacter CC pylori (ulcers and gastric cancer). It may be of particular CC use before insertion of an in-dwelling device or any other CC invasive procedure. The protein, or nucleic acid encoding CC invasive procedure. The protein, or nucleic acid encoding CC antibacterials. The DNA may also contain flanking sequences CC that are potential sources of control elements for bacterial CC gene expression. Detecting a sequence encoding the protein CC can be used diagnostically, e.g. to detect a mutation for CC can be used diagnostically, e.g. to detect a mutation for CC commence 7940 An.
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Best Local
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δõ
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae encoded polypeptide coding region; ORF; open reading frame; antib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W60976 standard; Protein; 299 AA
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WPI; 98-286586/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acids from Streptococcus pneumoniae - useful, e.g. for identifying anti-bacterial(s) for treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Black MT, Hodgson JE,
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27-OCT-1997; U19226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection;
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                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 21; Conser
                                                                             14 NYDKKKLLTHQGESIENRFxKEGNQLPDEFVVxERKKRSLSTNTS-DIXVTATNDSRLYP 72
                                                                                                                  38 dystnaifdhhgqakvslfakeagvlag-ltvfqrvftlfdaevtfqnphqfkdgdrlts 96
                                      97 gdl-vl-eiig-svrslltcervalnflqhlsgiasmtaayve 136
GALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLAS-SDSFLQ 114
                                                                                                                                                                                   3.3%;
Similarity 21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prevention; meningitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knowles DJC, Lonetto MA, Nicholas RO
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Pred. No. 1.12e+01
20; Mismatches 1
                                                                                                                                                                  Score 108; DB 33;
Pred. No. 1.12e+01;
35; Mismatches 40
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                                                                                                                                                                    Mismatches 40; Indels
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PR N-PSDB; V2493/.

Helicobacter pylori nucleic acid sequences and encoded Helicobacter pylori nucleic acid sequences and encoded problement pyloride(s) - useful in vaccines to treat or prevent H. pylori polypeptide(s) - useful in vaccine to prevent or treat H. pylori cellular protein.

CC This sequence is a H. pylori cellular protein.

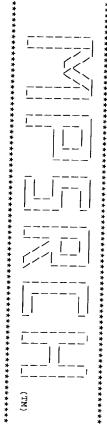
CC The protein may be used in a vaccine to prevent or treat H. pylori cellular protein are protein as potential H. pylori life cycle activators or inhibitors. The CC useful as potential H. pylori life cycle activators or inhibitors. The CC DNA and probes derived from it may be used for the identification of CC acid sequences complementary to the DNA act as antisense sequences and CC against the protein can be used in immunoassays to evaluate the abundance against the protein can be used in immunoassays to evaluate the abundance CC and distribution of H. pylori-specific antiquens. The genomic sequence of CC and distribution of H. pylori-specific antiquens. The genomic sequence of CC and distribution of H. pylori-specific antiquens. The genomic sequence of CC and colly shearing the bacterial DNA. The sequences were analysed CC interest, particular regions and the predicted coding regions for CC defined by computer evaluation. To identify likely H. pylori antiquens for vaccine development, the amino acid sequences predicted from various ORF content of the proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
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  DT KW KW PR PR PR PR
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29-MAR-1996;
02-APR-1996;
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H. pylori ORF 29ge30321_24336712_f1_5 cellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori.
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Alm RA, Smith D;
WPI; 97-503122/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                W61278 standard; Protein; 527 AA. W61278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hosts
                                                                                                                                      Monamine oxidase A; abnormal behaviour; serotonin;
                                                                           US5783680-A.
                                                                                                               noradrenaline; mental retardation; impulsive aggression
(GEHO ) GEN HOSPITAL CORP
                       06-OCT-1993; 132168.
06-OCT-1993; US-132168.
                                                                                                  Homo sapiens.
                                                                                                                                                                               29-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                 270 V 270
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                                                                                                                                                                                                                                                                                                                                                                        210 PGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGRQVYLKLETTSKSXEVEAAFEALIKG 269
                                                                                                                                                                                                                                                                                                                                                                                                                      325
                                                        21-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                psslmrdsvsledskkr-lnaikdlifhknkaf-rqlqlklntplkal-veaqkdgefka 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.38;
Similarity 34.48;
21; Conservation
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US-625811.
US-758731.
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Best Local (
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MAO-A catalyses oxidative deamination of dietary amines and neurotransmitters, eg. dopamine. The product may be used to develop therapeutic inhibitors, to metabolise dietary monoamines or to act a ferrometabolise.
                                                                                                                                                                                                                                                                                                                                          Purified DNA encoding human monoamine oxidase type A - used to detect eg. MAO-A alterations, associated with manic depression, and expressed to form MAO inhibitors to treat psychotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human monoamine oxidase type A gene product.
Muman monoamine oxidase type A; MOA-A; mental retardation;
manic depression; psychotic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mono:amine oxidase enzyme

Disclosure; Column 47-50; 30pp; English
A genetic defect linked to pl1-p21 of the x chromosome, especially
mutation C936T in exon 8 of the monamine oxidase (MAD) gene is related
abnormal behaviour. MAD metabolises serotonin, dopamine and
noradrenaline, neurotransmitters whose metabolism is known to affect
behaviour. Disregulation of these transmitters leads to borderline
mental retardation and abnormal behaviour (including impulsive
aggression). Probes based on the mutated sequence can be used for the
                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                       false transmitters.
                                                                                                                                                                                                                                                                                                                                    disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                          Breakefield X; WPI; 90-037130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R05079 standard; protein; 527 AA. R05079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-1989; 02901.
30-JUN-1988; US-213544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9000195-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-1993 (revised)
11-JUL-1990 (first en
310 VEDLIQEGSRFTADHPGLPISYTTSFLRDNV-VATFQNSTDYVETKVTAYRNGDLLLDHS 368
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Sequence 527 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYKA-) UNIV STICHTING KATHOLIEKE.
Breakefield XO, Brunner HG;
WPI; 98-427102/36.
N-PSDB; V27798
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                                  60 v-dyvdvggayvgptqnrilrlskelgietykvnvserlvqyvkgktypfrgafppvwnp 118
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                                                                                                      1 mengekasiaghmfdvvvigggisglsaak-llteygvsvlvleardrvggrtytirneh 59
                                                                                                                                                Match 3.1%;
Local Similarity 19.3%;
es 29; Conservative
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                                                                      LETTSKSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVTGKVDM 309
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                                                                                                                                            Score 99; DB 2; Length 527; Pred. No. 4.32e+01; 40; Mismatches 75; Indels
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Pred. No. 4.32e+01;
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Search completed: Mon Aug 30 16:04:20 1999 Job time : 114 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Mon Aug 30 16:01:21 1999; MasPar time 20.82 Seconds 906.662 Million cell updates/sec

Description: Perfect Score: Title: >US-09-120-044-3-COPY (1-471) from devil20044.pep 3241 1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Sequence:

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 50.333; Variance 110.368; scale 0.456

SUMMARIES

222118 232118 3422118 3532118	Result No.
1599 1542 1532 1532 1476 1476 1476 1475 1475 1741 1741 1741 1741 1741 1741	Score 3239
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ALIGNMENTS

	PGALLVVDETLXEN	XVTATNDSRL	Qy 61	~
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	LAMNYDKKKLLTHQG	MANKAVNDFI	0у 1	~
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ative 1; Mismatches 8; Indels 0; Gaps 0;	rvative	462; Cc	Matches	
	99.9%;	Query Match Best Local Similarity	Query Match	
<pre>#product pneumolysin #status predicted #label MAT #length 471 #molecular weight 52899 #checksum 8274</pre>	#product pneu ngth 471 #mole	# <u>1</u> e	2-471 SUMMARY	
##CTPOSS-references EMBL:X52474, NID:947403; PID:947404 FICATION #superfamily dipeptide transport protein E	ences EMBL:x5247	ross-refere	##CTOSS- CLASSIFICATION FEATURE	
DNA 1-471 ##label MIT	pe DNA 1-471 ##label	#molecule_type	###nc	
1	S12829	n	######################################	
cross-references MUID:90326546	MUID: 90326546	-reference	#cross	
genes and pro	nparison of pneu	Col	#title	
Acids Res. (1990) 18:4010	cleic Acids Res.		#journal	
MICCHEIL, T.J.; Mendez, F.; Paton, J.C.; Andrew, P.W.; Boulnois, G.J.	Boulnois, G.J. Me		# du CIOL 8	
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Sulinydryl-activated toxin of Streptococcus pneumoniae.	sulinydryl-activ s MUTD:87193109	-reference	#cross	
sequence of the gene for pneumolysin, the	sequence of the			
and complete	lecular cloning,	МС	#title	
1987) 55:1184-1180	fect. Immun. (19		#journ	
Walker, J.A.; Allen, R.L.; Falmagne, P.; Johnson, M.K.;	lker, J.A.; Alle		#authors	
512829	A28568; S12829		REFERENCE	
7-1998	21-Aug-1998		ACCESS TON	
1988	-Nov-1988 #seque	19	DATE	
pneumolysin - Streptococcus pneumoniae	eumolysin - Str	ď.	TITLE	
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                                                                                                                     GENETICS
SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                   #journal Infect. Immun. (1988) 56:3235-3240
#title Nucleotide sequence of the gene for perfringolysin 0
    (theta-toxin) from Clostridium perfringens: significant homology with the genes for streptolysin 0 and pneumoly:
#cross-references MUID:89032623
                                                                                                                                                                                                              #title Cloning and expression in Escherichia coli of the perfringolysin 0 (theta-toxin) gene from Clostridium perfringens and characterization of the gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references MUID:91099951
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                                                                                                                                                                                                                                                                                                                                                                                       ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-500 ##label SHI 1-500 ##label SHI ##cross-references GB:M81080; NID:g144885; PID:g144886 ##note translation of the nucleotide sequence is not complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA
                                                                                                                                      ##experimental_source ATCC 13124
                                                                                                                                                             ##residues
                                                                                                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
                                                                                                                                                             ##molecule_type protein
##residues 29-45 ##label TW2
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A43577
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perfringolysin O precursor - Clostridium perfringens
#formal_name Clostridium perfringens
03-Feb-1993_#sequence_revision 03-Mar-1993 #text_change
                                                                                                                                                                                                 A60922
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#length 500
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                                    #domain signal sequence #status predicted #label SIG\
#product perfringolysin O #status experimental #label
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#molecular-weight 55799
      #checksum 4821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal Infect. Immun. (1988) 56:766-772
#title Expression in Escherichia coli and sequence analysis of the listeriolysin O determinant of Listeria monocytogenes.
#cross-references MUID:88153053
                                                                                                                                                                 #authors Domann, E.; Chakraborty, T.
#journal Nucleic Acids Res. (1989) 17:6406
#title Nucleotide sequence of the listerioly
monocytogenes serotype 1/2a strain.
#cross-references_MUID:89366684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors
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Local Similarity 46.5%;
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                                                                                                                                                                                                                                                                                                                            ##residues 1-529 ##label MEN
##cross-references GB:M24199; NID:g149652; PID:g149653
##note this sequence is derived from a strongly hemolytic
                                         ##note
                                                         ##experimental_source strain EGD
                                                                              ##cross-references EMBL:X15127;
                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type DNA
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                                                                                                          ##residues
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listeriolysin O precursor - Listeria monocytogenes
#formal_name Listeria monocytogenes
21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                           A43505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mengaud, J.; Vicente, M.F.; Chenevert, J.; Pereira, J.M.;
Geoffroy, C.; Gicquel-Sanzey, B.; Baquero, F.; Perez-Diaz,
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                serotype 1/2a
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Pred. No. 1.85e-270;
                                                                                     NID:g44106; PID:g44107
                                                                                                                                                                                                                      listeriolysin gene from a Listeria
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                                                                                                                                        425
                                                                                                                                                                 481 AKECTGLAWEWWRTVIDDRNLPLVKNRNISIWGTTLYPKYSNKVDN 526
                                                                                                                                                                                                                                                                 421 IDHSGGYVAQFNISWDEVNYDPEGNEIVQHKNWSENNKSKLAHFTSSIYLPGNARNINVY 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AVNDLLAKWHQDYGQVN-NVPARXQYEKTTAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AVNTLVERWNEKYAQAYPNVSAKIDYDDEMAYSESQLIAKFGTAFKAVNNSLNVNFGAIS 240
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                                                                                                                         IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN 470
                                                                                                                                                                                                                                                                                                               GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL 364
                                                                                                                                                                                                                                                                                                                                                                                                            QVYLKLETTSKSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGR
                                                                                                                                                                                                                    LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n 47.6%; Score 1542; DB 2; Similarity 42.9%; Pred. No. 1.62e-259;
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Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtained by single amino acid substitutions in listeriolysin O.
            listeriolysin
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#product listeriolysin O #status predicted #label MAT
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Identification of the structural gene encoding the SH-activated hemolysin of Listeria monocytogenes:
listeriolysin O is homologous to streptolysin O and
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                                                                                                                                                  425 IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN 470
                                                                                                                                                                       481 AKECTGLAWEWWRTVIDDRNLPLVKNRNISIWGTTLYPKYSNSVDN 526
                                                                                                                                                                                                                                  365 LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
                                                                                                                                                                                                                                                                       421 IDHSGGYVAQFNISWDEINYDPEGNEIVQHKNWSENNKSKLAHFTSSIYLPGNARNINVY 480
                                                                                                                                                                                                                                                                                                                                                        361 GNLGDLRDILKKGATENRETPGVPIAYTTNELKDNELAVIKNNSEYIETTSKAYTDGKIN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                       301 QVYLKLSTNSHSTKVKAAFDAAVSGKSVSGDVELTNIIKNSSFKAVIYGGSAKDEVQIID 360
                                                                                                                                                                                                                                                                                                                                                                                               245 QVYLKLETTSKSXEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 SGEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 AVNDLLAKWHQDYGQVN-NVFARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 EGKMQEEVISFKQIYYNVNVNEPTRPSRFFGKAVTKEQLQALGVNAENPPAYISSVAYGR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AVNTLVERWNEKYAQAYPNVSAKIDYDDEMAYSESQLIAKFGTAFKAVNNSLNVNFGAIS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ISSLTYPGALVKANSELVENQPDVLPVKRDSLTLSIDLPGMTNQDNKIVVKNATKSNVNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##cross-references EMBL:X60035; NID:g44110; PID:g44112
##experimental_source strain 12067, serotype 4b
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                                                                                                                                                                                                                                                                                                                 GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
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Similarity 42.7%;
S22341 #type complete
ivanolysin precursor - Listeria ivanovii
#formal_name Listeria ivanovii
07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain signal sequence #status predicted #label SIG\
#product listeriolysin #status predicted #label MAT
#length 529 #molecular-weight 58887 #checksum 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 117; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rasmussen, O.F.; Beck, T.; Olsen, J.E.; Dons, L.; Infect. Immun. (1991) 59:3945-3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
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strain 12067
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Pred. No. 3.58e-258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVNDLLAKWHQDYGQVN-NVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
                                                                                                                                                                                                       | IRECTGLAWEWWRTVYEKTDLPLYRKRTISIWGTTLYPQVEDKVEN 470
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Similarity 42.98;
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S22340
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submitted to the EMBL Data Library,
S36683
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Biochim. Biophys. Acta (1992) 1130:81-84
Listeriolysin genes: complete sequence of ilo from Listeria
ivanovii and of 1so from Listeria seeligeri.
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#product ivanolysin #status predicted #label MAT
#length 528 #molecular-weight 58511 #checksum 6874
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                                                         $22340 #type complete
seeligeri
#formal_name Listeria seeligeri
22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change
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                                        21-Aug-1998
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 QYYYKLSSSSHSNKYKTAFEAAMSGKSYKGDVELTNIIKNSSFKAVIYGGSAKEEVEIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 AVNDLLAKWHQDYGQVN-NVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 AVNTLVERWNDKYSKAYPNINAKIDYSDEMAYSESQLIAKFGTAFKAVNNSLNVNFEAIS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ISSLTYPGALVKANRELVENOPNVLPVKRDSLTLSVDLPGMTKKDNKIFVKNPTKSNVNN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 DGKVQEEVISFKQIYYNINVNEPTSPSKFFGGSVTKEQLDALGVNAENPPAYISSVAYGR 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     y Match 45.5%; Score 1476; DB 2; Length 53
Local Similarity 42.5%; Pred. No. 7.35e-247;
hes 198; Conservative 111; Mismatches 156; Indels
##residues 1-501 ##label GEO
##cross-references GB:M62709; NID:g142472; PID:g142473
y #length 501 #molecular-weight 55268 #chec
                                                                     ##molecule_type DNA
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                                                                                               ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDHSGGYVAQFNISWDEVSYDENGNEIKVHKKWGENYKSKLAHFTSSIYLPGNARNINIY 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVYLKLETTSKSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL}
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Biochim. Biophys. Acta (1992) 130:81-84
Listeriolysin genes: complete sequence of ilo from Listeria
ivanovii and of 1so from Listeria seeligeri.
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#length 530 #molecular-weight 59181 #c
                                                                                                                                                                                                             J. Bacteriol. (1990) 172:7301-7305
Alveolysin, the thiol-activated toxin of Bacillus alvei,
homologous to listeriolysin O, perfringolysin O,
                                                                                                                                                                                                                                                                                                                                                                      alveolysin - Bacillus alvei
#formal_name Bacillus alvei
28-Jun-1991 #sequence_revision
                                                                                                                       A37858
                                                                                                                                                                                                                                                        Geoffroy, C:; Mengaud, J.; Alouf, J.E.; Cossart, J. Bacteriol. (1990) 172:7301-7305
                                                                                                                                                                                   pneumolysin, and streptolysin O and contains a single
                                                                                                                                                                cysteine
                                                                                                                                             MUID:91072294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #authors
169 VTDRTYPAALQLANKGFTENKPDAVVTKRNPQKIHIDLPGMGDKAT-VEVNDPTYANVST 227
                                                                                                                                                                   109 INDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIERKKKNINTTPVDISIIDS 168
                                                                                                                                                                                                                                                                                    ##residues 1-571 ##label_KEH
##cross-references GB:M18638; NID:g153810; PID:g153811
# #length 571 #molecular-weight 63638 #chec
                                                                                                                                                                                                                                                                                                                                          ##molecule_type DNA
##rosia...-
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                                                    66 NDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 GLAWEWWRTVVDEYNVPLASDINVSIWGTTLYP 495
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Local Similarity 41.9%;
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                                                                                                                               6 VNDFILAMNYDKKKLLTHQGESIENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVTAT 65
                                                                                                                                                                                                                                                          Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQSVIKDNAQFSSKNPAYPISYTSVFLKDNSIAAVHNNTEYIETKTTEYSKGKIKLDHSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGRQVYLK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VMVAAYKQIFYTVSAGLPNNPSDLFDDSVTFAELARKGVSNEAPPLMVSNVAYGRTIYVK 282
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                                                                                                                                                                                                           ch 43.7%; Score 1415; DB 2; 1
1 Similarity 42.0%; Pred. No. 3.52e-235;
192; Conservative 104; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A43507 #type complete
streptolysin O precursor - Streptococcus pyogenes
#formal_name Streptococcus pyogenes
28-oct-1992 #sequence_revision 28-oct-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                             A43507
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the streptolysin O (SLO) structural homologies between SLO and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
                           343 KDFNEIRNIIKDNAELSFKNPAYPISYTSTFLKDNATAAVHNNTDYIETTTTEYSSAKMT 402
                                                                                                                                                                                         185
                                                                                                                                                                                                                     223 NGEKKYMVAAYKQIFYTVSAELPNNPSDLFDNSVTFGELTRKGVSNSAPPVMVSNVAYGR
                                                                                                                                                                                                                                                                              125
                                                                                                                                                                                                                                                                                                        163 GAVDDLYSTWNEKYSATHTLPARMQYTESMYYSKAQIASALNYNAKYLDNSLNIDENAVA 222
                                                                                                                                                                                                                                                                                                                                                                                                  104 SVANRTYPGAVQLANKAFADNQPSLLVAKRKPLNISIDLPGMRKENT-ITVQNPTYGNVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##cross-references GB:D21270; NID:g418066; PID:g600252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 VYLKLETTSKSxEVEAAFEÄLIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVTG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 VFVKLETSSKSNDVEAAFSAALKGTDVKTNGKYSDILENSSFTAVVLGGDAAEHNKVVTK 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 GEKQIQIYNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQ
                                                                                                                                                                                                                                                                                                                                                        65 TNDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVR 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 GEKKYMIAAYKQIFYTYSANLPNNPADVFDKSVTFKELQRKGVSNEAPPLFVSNVAYGRT 347
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GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                                 TVYVKLETTSKSKDVQAAFKALLKNNSVETSGQYKDIFEESTFTAVVLGGDAKEHNKVVT
                                                                                       QVYLKLETTSKSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                                                           SGEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGR 244
                                                                                                                                                                                                                                                                   GAVNDLLAKWHQDYGQVNNVPARxQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
                                                                                                                                                                                                                                                                                                                                                                                                                                              AVNDFILAMNYDKKKLLTHQGESIENRFxKEGNQLPDEFVVxERKKRSLSTNTSDIXVTA 64
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Infect. Immun. (1994) 62:4000-4004
The gene encoding a new mitogenic factor in a Streptococcus pyogenes strain is a distributed only in group A
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19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
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hemolysin - Bacillus cereus (fragment)
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Best Local Similarity 33.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-112 ##label SEG
##cross-references EMBL:236908; NID:g535307; PID:g535308
##cross-references EMBL:236908; NID:g535307; PID:g535308
                                                                                                                                                                                                                                                                                                                               ##cross-references EMBL:236907; NID:g535305; PID:g535306
yr #length 96 #molecular-weight 10471 #checksu
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                                                                                                             64 ATNDSRLYPGALLVVDETLXENNPTLLAV 92
                                                                                                                                              61 XAKAANISPGALLRAXQNLLDNNPTLISI 89
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                                                                                                                                                                                                                       KQDNQYFQSLTYGPQEILTNEGEYIDNPPATTGMLENGRFVVLRREKXTITDNSADITVI 60
                                                                                                                                                                                    KAVNDFILAMNYDKKKLLTHQGESIENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVT 63
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S47297
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#formal_name Streptococcus suis
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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suilysin - Streptococcus suis
#formal_name Streptococcus suis
06-Jan-1995_#sequence_revision 06-Jan-1995 #text_change
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larity 50.9%;
Conservative
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monoamine oxidase type A
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ase (flavin-containing) (EC 1.4.3.4)
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Pred. No. 2.01e-57;
22; Mismatches 33
                                                                                                                                                                                                                                                           Score 214; DB 2; Length 96; Pred. No. 3.17e-15; 23; Mismatches 36; Indels
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Best Local Similarity 20.0%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #title The primary structure of bovine monoamine oxidase type A.
Comparison with peptide sequences of bovine monoamine
oxidase type B and other flavoenzymes.
#cross-references MUID:89248344
#accession S03974
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                                                                    #journal J. Biol. Chem. (1991) 266:6416-6423

#title The MAS-encoded processing protease of yeast mitochondria.

Interaction of the purified enzyme with signal peptides
a purified precursor protein.

#cross-references_MUID:91177897
                                                                                                                                                                                                                                                                                                                                                 #title MAS1, a gene essential for yeast mitochondrial assembly, encodes a subunit of the mitochondrial processing protease. #cross-references_MUID:88312592
                                                                                                                                                                                                             #authors
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DS FAD; flavoprotein; mitochondrion; oxidoreductase
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##molecule_type protein
##residues 21-32 ##label YAN
                                                                                                                                                                                                                                                              ##cross-references EMBL:X07649; NID:g3886; PID:g3887
                                                                                                                                                                                                                                                                                                     ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - yeast (Saccharomyces cerevisiae) mitochondrial processing proteinase 48K chain; processing enhancing protein; protein L9632_10; protein
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28.Feb-1990 #sequence_revision 28-Feb-1990 #text_change
                                                A38734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #length 527 #molecular-weight 59800 #checksum 6598
                                                                                                                                                                                     Yang, M.; Geli, V.; Oppliger, W.; Suda, K.; James, Schatz, G.
                                                                                                                                                                                                                                                                                                                                                                                                                         Witte, C.; Jensen, R.E.; Yaffe, M.P.; Schatz, EMBO J. (1988) 7:1439-1447
                                                                                                                                                                                                                                                                                                                                     S0055
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#modified_site S-(8alpha-FAD)-cysteine (Cys) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not compared with conceptual translation
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                                                                                                                                                                                                                                                                                         1-462 ##label WIT
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Pred. No. 1.66e-02;
Pred. "---+ches 72;
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SUMMARY
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ENTRY
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       Query Match
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Best Local :
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                                                         #map_position
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                                                                                                             ##cross-references EMBL:273307; NID:g1360550;
MIPS:YLR135w
                                                                                                                                                                 ##molecule_type DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 ILSDILTKSVLDNSAIERERDVIIRESEEVDKMYDEVVFDHLHEITYKDQPLGRTILGPI 184
                                                                                                                                                                                                                                                                ##experimental_source strain S288C
                                                                                                                                                                                                                                                                           ##cross-references EMBL:X91258; NID:g995686; PID:g995701
                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
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                                                                                              ##experimental_source strain S288C
                                                                                                                                                      ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 KNIKSITRTDLKDYITKNYKGDRMVLAG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references SGD:S0004153; MIPS:YLR163c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TAHELEHLAFK-GTQ-NRSQQGIELEIENI-GSHLNAYTSRENTVYYAKSLQEDIPKAVD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 3.5%;
Local Similarity 23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFQDTVTVEDLKQRGISAERPLVYI-Sx-VA--YGRQVYLKL-ETTSKSXEVEAAFEALI 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGYKVAPQTEWKQ-ILDNTEVKAVILGG 294
                   12R
#length 748 #molecular-weight 84361 #checksum
                                                                                                                                                                                       Delius, H.; Hebling, U. submitted to the Protein Sequence Database, May 1996 864977
                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, June 1995
36.8 kb of S.cerevisiae chromosome XII including ACE2, CKI1,
PDC5, SLS1, PUT1 and tRNA-Asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein L3140
#formal_name Saccharomyces cerevisiae
29.Nov-1995_#sequence_revision 23.Feb-1996 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                             Delius, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                    S59313
                                                                                                                                                                                                                                                                                                                                                                                                                                                 S59327; S64977
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hypothetical protein YLR135w -
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heterodimer; hydrolase; metalloproteinase; mitochondrial
matrix; mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #length
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#product mitochondrial processing peptidase beta chain #status experimental #label MAT
                                                                                                                                                1-748 ##label DEW
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       3.50;
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   Score 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 114; DB 1; Length 462;
Pred. No. 2.64e-01;
44; Mismatches 60; Indels
 ВВ
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                                                                                                                           PID:e245572; PID:g1360551;
Length 748;
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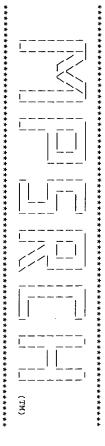
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #journal #title
                                                                                                                                                                                                                                                                                                                     #gene
                                                                                                                                                                                                                                                                                                                                                                                                                                      #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                   #cross-references MUID:94320770
                               314 NIPFALNTADVSLSTDGKTITVDASTPFENNTEYKVVVKGIKDKNG 359
318 S-RFTADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG
                                                                                                                                             200 YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGRQVYLKLETTSKSXEV 259
                                                                                                                                                                               200 YDITV-AMKAR-EV-QDAVKAGNLDKAKAAVDQINQYLPKVTDAFKTELT-EVAKKALDA 255
                                                                                                                                                                                                                                                                                                                                                  ##molecule_type DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  685 FDHLTELIEAFPDFLERIYTFEPIPLNELIEKLFSAEPFVSQIDEMTIREWADVQG 740
                                                                      260 -EAAFEALIKGVKVAPQTEWKQI-LDNTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEG
                                                                                                         256 DEAALTPKVESVS-AINTQNKAVELTAVPVNGT-LKLQLSAAANEDTVNVNTVRIYKVDG 313
                                                                                                                                                                                                                                                                                                                                                                                                                    ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  567 SEEEETEFDDQFCIADIQLVDSSKISTKDSTQNPTTSNDIIDTSAASSIASPEKFCEIMM 626
                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DETLXENNPTLLAVDRAPMTYSIDL-PGLASSDSFLQVEDPSNSSVRGAVNDLLAKWHQD 137
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33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuen, B.; Sleytr, U.B.; Lubitz, W.
Gene (1994) 145:115-120
Sequence analysis of the sbsA gene encoding the 130-kDa
surface-layer protein of Bacillus stearothermophilus strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I40468 #type complete
surface layer protein sbsA - Bacillus stearothermophilus
#formal_name Bacillus stearothermophilus
12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
18-Cct-1996
                                                                                                                                                                                                                       3.5%;
larity 24.1%;
Conservative
                                                                                                                                                                                                                                                                                                                       sbsA
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                                                                                                                                                                                                                                                                                                                                                                                                          preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                         Score 114; DB 2; Length 1228; Pred. No. 2.64e-01;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Run on: Mon Aug 30 15:58:43 1999; MasPar time 14.67 Seconds 907.846 Million cell updates/sec

Sequence: Description: Perfect Score: >US-09-120-044-3-COPY (1-471) from devil20044.pep 3241 1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: РАМ 150 Gap 11

Post-processing:

77977 seqs, 28268293 residues

Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 51.515; Variance 97.371; scale 0.529

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dФ					
Result No.	Score	Query Match	Length	88	ID	Description	Pred. No.
1	3228	99.6	470	<u>- </u>	TACY_STRPN	PNEUMOLYSIN (THIOL-ACT	0.00e+00
2	1599		500	ш		SI.	0.00e+00
ω	1542	47.6	529	ш	TACY_LISMO		1.20e-300
4	1523		528	μ.	TACY_LISIV	IVANOLYSIN PRECURSOR (2.01e-296
₅	1476	45.5	530	Ь	TACY_LISSE	SEELIGERIOLYSIN PRECUR	5.56e-286
0	1468	45.3	501	ш	TACY_PAEAL	ALVEOLYSIN PRECURSOR (.32€
7	1415	43.7	571	Н	TACY_STRPY	STREPTOLYSIN O PRECURS	1.91e-272
8	1416	43.7	574	ب	TACY_STREQ	0	1.14e-272
9	1399	43.2	574	ם	TACY_STRCB	STREPTOLYSIN O PRECURS	.71e
10	1336		485	ب	TACY_BACCE	HEMOLYSIN PRECURSOR (F	Ġ
11	124		527	ب	AOFA_BOVIN	AMINE OXIDASE [FLAVIN-	
12	114		462	_	MPPB_YEAST	MITOCHONDRIAL PROCESSI	.17e
13	114		1228	ш	SLAP_BACST	S-LAYER PROTEIN PRECUR	5.17e-02
14	106		511	-	NOP5_YEAST	NUCLEOLAR PROTEIN NOP5	٠
15	104	3.2	364	ш	GCH2_PHOLE	GTP CYCLOHYDROLASE II	
16	105		418	ᆫ	Y285_HELPY	HYPOTHETICAL PROTEIN H	7.42e-01
17	104		504	\vdash	FLIC_SALMU	FLAGELLIN (PHASE-1-D F	9.87e-01
18	105		514	Н	THD1_SALTY	THREONINE DEHYDRATASE	7.42e-01
19	100	3.1	146	۲	CASK_UNCUN	KAPPA CASEIN (FRAGMENT	3.02e+00
20	100		279	ب	YRR6_MYCCA	HYPOTHETICAL 33.0 KD P	ω.
21	99	3.1	340	Ь	HYPE_RHOCA	HYDROGENASE EXPRESSION	3.98e+00
22	99	3.1	350	ب	ARGI_SOYBN	ARGINASE (EC 3.5.3.1).	3.98e+00
23	100	3.1	427	_	GLYA_SYNY3	SERINE HYDROXYMETHYLTR	3.02e+00

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
98	97	97	97	97	97	96	96	97	98	100	99	100	99	101	99	102	101	99	100	100	100
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CLH_RAT	BGAL_STRTR	A4_MOUSE	A4_RAT	GR78_APLCA	Y223_MYCPN	NEUS_MOUSE	PHOL_MYCLE	SBCD_BACSU	RAS1_YEAST	TANA_XENLA	CLH_CAEEL	CYA4_TRYBB	MFD_BACSU	V120_HSV11	SYV_METJA	Y328_MYCGE	YG42_YEAST	AOFA_HUMAN	YJIV_ECOLI	SPE1_LYCES	FLIC_SALRU
Ħ,	OSIDASE (ALZHEIMER'S DISEASE AM	78 KD GLUCOSE REGULATE	HYPOTHETICAL PROTEIN M	NEUROSERPIN PRECURSOR	PHOH-LIKE PROTEIN.	EXONUCLEASE SBCD HOMOL	RAS-LIKE PROTEIN 1.	TANABIN.	PROBABLE CLATHRIN HEAV	RECEPTOR-TYPE ADENYLAT	TRANSCRIPTION-REPAIR C	CAPSID ASSEMBLY PROTEI	VALYL-TRNA SYNTHETASE	HYPOTHETICAL PROTEIN M	HYPOTHETICAL 78.8 KD P	AMINE OXIDASE [FLAVIN-	HYPOTHETICAL 58.2 KD P	ARGININE DECARBOXYLASE	FLAGELLIN (PHASE-1-R F
5.22e+00	6.83e+00	6.83e+00 ·	6.83e+00	6.83e+00	6.83e+00	8.91e+00	8.91e+00	6.83e+00	5.22e+00	3.02e+00	3.98e+00	3.02e+00	3.98e+00	2.29e+00	3.98e+00	1.74e+00	2.29e+00	3.98e+00	3.02e+00	3.02e+00	3.02e+00

ALIGNMENTS

RESULT	1
AC.	P11990;
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ΡŢ	01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE)
ΡŢ	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN).
GN	PLY.
SO	STREPTOCOCCUS PNEUMONIAE.
8	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
8	STREPTOCOCCUS.
RN	[1]
₽₽	SEQUENCE FROM N.A.
RC	STRAIN=NTCC 7466 SEROTYPE II;
RX	MEDLINE; 87193109.
RA	WALKER J.A., ALLEN R.L., FALMAGNE P., JOHNSON M.K., BOULNOIS G.J.;
RT	and complete nucleotid
RT	sequence of the gene for pneumolysin, the sulfhydryl-activated toxin
RT.	of Streptococcus pneumoniae.";
æ	INFECT. IMMUN. 55:1184-1189(1987).
റ്റ	-!- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL
റ്റ	CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.
S	CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
දු	EUKARYOTIC CELL MEMBRANES.
ဌ	-!- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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8	the European Bioinformatics Institute. There are no restrictions on its
-	use by non-profit institutions as long as its content is in no way

STEWN DRANGE CCC INIT_MET ACT_SITE SEQUENCE EMBL; X52474; G47404; -.
EMBL; M17717; G153692; -.
PIR; A28568; A28568.
PROSITE; PS00481; THIOL_CYTOLYSINS; 1.
PFAM; PF01289; Thiol_CYTOLYSIn; 1.
HSSP; P19995; 1PFO.
TOXIN, HEMOLYSIS; CYTOLYSIS. use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 0 427 470 AA; 427 I 52768 MW; BINDING TO CHOLESTEROL (BY SIMILARITY).; D3F3A252 CRC32;

Query Match 99.6%; Score 3228; DB 1; Best Local Similarity 98.1%; Pred. No. 0.00e+00; Length 470;

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                                                                         OHNO-IWASHITA Y., IWAMOTO M., MI "Cold-labile hemolysin produced from Clostridium perfringens.";
                                                                                                                                                                                                                                                     "Nucleotide sequence of the gene for perfringolysin O (theta-toxin) from Clostridium perfringens: significant homology with the genes f streptolysin O and pneumolysin."; INFECT. IMMUN. 56:3235-3240(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91099951.
SHIMIZU T., OKABE A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (REL. 17, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
PERFRINGOLYSIN O PRECURSOR (THETA-TOXIN) (THIOL-ACTIVATED CYTOLYSIN).
PEO OR PEOR OR PEOA.
        SEQUENCE
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                                                                                                                                                                                                               SEQUENCE OF 29-45
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"An upstream regulatory sequence stimulates expression of perfringolysin O gene of Clostridium perfringens.";
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492-500 FROM N.A.
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-!- SUBUNIT: FORMS OLIGOMERS IN THE HOST MEMBRANE.
-!- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00481; THIOL_CYTOLYSINS; 1. PFAM; PF01289; Thiol_Cytolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL 89:685-692(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE: 97325744.

ROSSJOHN J., FEIL S.C., MCKINSTRY W.J., TWETEN R.K., "Structure of a cholesterol binding, thiol-activated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium perfringens: beta-galactosidase the 3'-flanking region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRALM-NCTC 8237;
MEDLINE; 96123363.
SHMIZU T., KOBANASHI T., BA-THEIN W.,
"Sequence analysis of flanking regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              model of its membrane form.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEIL S.C., ROSSJOHN J., ROHDE K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from Clostridium perfringens.";
EUR. J. BIOCHEM. 167:425-430(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MICROBIOL. IMMUNOL.
              154 VSGAIDELVSKWNEKYSSTHTLPARTQYSESMVYSKSQISSALNVNAKVLENSLGVDFNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Crystallization and preliminary X-ray analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EBS LETT. 397:290-292(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WAMOTO M., OHNO-IWASHITA Y.,
"Role of the essential thiol"
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                                                                                                                                                        NKAVNDFILAMNYDKKKLLTHQGESIENRFxKEGNQLPDEFVVxERKKRSLSTNTSDIxV
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D -> K (IN REF. 3).
K -> I (IN REF. 3).
RKP -> EA (IN REF. 2).
RKP -> EA (IN REF. 2).
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Pred. No. 0.00e+00;
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TED BY OXIDATION.
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P13128; Q48747; Q57096; Q57206;
O1-JAN-1990 (REL. 13, CREATED)
O1-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 13, LAST ANNOTATION UPDATE)
LISTERIOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
HLY OR LISA OR HLYA.
                                                                                                    VINES A., SWAMINATHAN B.;

SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-i- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.

CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.
                                                                                                                                                                                                                                                                "RASMUSSEN O.F., BECK T., OLSEN J.E., DONS L., ROSSEN L.;
"Listeria monocytogenes isolates can be classified into two i
types according to the sequence of the listeriolysin gene.";
INFECT. IMMUN. 59:3945-3951(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                         MENGAUD J. VICENTE M.-F., CHENEVERT J., PEREIRA J.M., GE
GICQUEL-SANZEY B., BAQUERO F., PEREZ-DIAZ J.-C., COSSART
"Expression in Escherichia coli and sequence analysis of
listeriolysin O determinant of Listeria monocytogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence of the listeriolysin monocytogenes serotype 1/2a strain."; NUCLEIC ACIDS RES. 17:6406-6406(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=EGD / SEROTYPE 1/2A;
MEDLINE; 89366684.
   the
                                                                                                                                                                                                              STRAIN-F2365, F5782 (SEROTYPE 4B), AND F4233,
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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inis SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the EMPL outstations on its content is in no way
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                                                                                     TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY
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TACY_LISIV STAN p31831; 01-JUL-1993 (REL. 2 01-JUL-1993 (REL. 2 15-JUL-1998 (REL. 3 IVANOLYSIN PRECURSO

STANDARD;

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3 (REL. 26, CREATED)
3 (REL. 26, LAST SEQUENCE UPDATE)
8 (REL. 36, LAST ANNOTATION UPDATE)
PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; 805306; 805306.
PIR; A43505; A43505.
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L; M24199; G149653; -.
L; X60035; G44112; -.
L; U25452; G887870; -.
L; U25443; G887016; -.
L; U25446; G887804; ALT_INIT.
L; U25449; G887864; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                  SGEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGR
                                                                                                                                                                                                                                                                                                                                                                                                  IDKYIQGLDYNKNNVLVYHGDAVTNVPPRKGYKDGNEYIVVEKKKKSINQNNADIQVVNA 120
IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN
                        AKECTGLAWEWWRTVIDDRNLPLVKNRNISIWGTTLYPKYSNKVDN 526
                                                                                                                                                                                   QVYLKLSTNSHSTKYKAAFDAAVSGKSVSGDVELTNIIKNSSFKAVIYGGSAKDEVQIID
                                                                                                                                                                                                                                                                                        AVNTLVERWNEKYAQAYPNVSAKIDYDDEMAYSESQLIAKFGTAFKAVNNSLNVNFGAIS
                                                                  IDHSGGYVAQFNISWDEVNYDPEGNEIVQHKNWSENNKSKLAHFTSSIYLPGNARNINVY
                                                                                                      GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                   GNLGDLKKGATFNRETPGVPIAYTTNFLKDNELAVIKNNSEYIETTSKAYTDGKIN
                                                                                                                                                          QVYLKLETTSKSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                                                                                                                       EGKMQEEVISFKQIYYNVNVNEPTRPSRFFGKAVTKEQLQALGVNAENPPAYISSVAYGR
                                                                                                                                                                                                                                                                  AVNDLLAKWHQDYGQVN-NVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
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                                                                                                                                                                                                                                                                                                                                                                         VNDFILAMNYDKKKLLTHQGESIENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVTAT
                                                    LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
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S -> L (IN STRAINS F2365, F4233, F5782,
F6789 AND 12067).

M -> I (IN STRAIN F2365).

V -> I (IN STRAINS F2365, F4233, F5782,
F6789 AND 12067).

K -> S (IN STRAINS F2365, F4233, F5782,
F6789 AND 12067).
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1542; DB 1;
Pred. No. 1.20e-300,
117; Mismatches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISTERIOLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269EA737 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
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Best Local S
Matches 19
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00481; THIOL_CYTOLYSINS PFAM; PF01289; Thiol_cytolysin; 1. HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X60461; E39053; ALT_INIT. PROSITE; PS00481; THIOL_CYTOLYSINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Listeriolysin genes: complete sequence of ilo from Listeria ivanovii and of lso from Listeria seeligeri."; BIOCHIM. BIOPHYS. ACTA 1130:81-84(1992).
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MEDLINE; 92182018.
HAAS A., DUMBSKY M., KREFT J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
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425 IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN
                                                                                                                                                                                                                                 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 LASLTYPGALVKANSELVENQPDVLPVKRDSVTLSIDLPGMVNHDNEIVVQNATKSNIND 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
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SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHÓLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
                                   AKECTGLAWEWWRTVVDDRNLPLVKNRNVCIWGTTLYPAYSDTVDN 525
                                                                                                         LDHSGAYVARFNVTWDEVSYDANGNEVVEHKKWSENDKDKLAHFTTSIYLPGNARNINIH 479
                                                                                                                                                GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                                                                                                                                                              DIFVKLSTSSHSTRVKAAFDTAFKGKSVKGDTELENIIQNASFKAVIYGGSAKDEVEIID 359
                                                                                                                                                                                                                                                                                                 SGEKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGR
                                                                                                                                                                                                                                                                                                                                                                             AVNDLLAKWHQDYGQVN-NVPARxQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                 GVNTLVDRWNNKYSEEYPNISAKIDYDQEMAYSESQLVAKFGAAFKAVNNSLNVNFGAIS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNDFILAMNYDKKKLLTHQGESIENRFxKEGNQLPDEFYVxERKKRSLSTNTSDIxVTAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDQYIQGLDYDKNNILVYDGEAVKNVPPKAGYKEGNQYIVVEKKKKSINQNNADIQVINS 119
                                                                        LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
                                                                                                                                                                                    GDLSKLRDILKQGANFDKKNPGVPIAYTTNFLKDNQLAVVKNNSEYIETTSKAYSDGKIN 419
                                                                                                                                                                                                                           QVYLKLETTSKSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                                                                                                                                                                                                                      EGKVQEEVINFKQIYYTVNVNEPTSPSRFFGKSVTKENLQALGVNAENPPAYISSVAYGR 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199;
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Similarity 42.7%;
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483
528 AA;
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483 B
58542 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1523; DB 1; 1
Pred. No. 2.01e~296;
119; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING TO CHOLESTEROL (BY SIMILARITY).; CFAE84AD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVANOLYSIN.
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P31830;
O1-JUL-1993 (REL. 2
O1-JUL-1993 (REL. 2
15-JUL-1998 (REL. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
ACT_SITE
SEQUENCE
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01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
SEELIGERIOLYSIN PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOXIN; HEMOLYSIS; CYTOLYSIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
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422
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                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AVNTLVERWNDKYSKAYPNINAKIDYSDEMAYSESQLIAKFGTAFKAVNNSLNVNFEAIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 ISSLTYPGALVKANRELVENQPNVLPVKRDSLTLSVDLPGMTKKDNKIFVKNPTKSNVNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 INKYIWGLNYDKNSILVYQGEAVTNVPPKKGYKDGSEYIVVEKKKKGINQNNADISVINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VNDFILAMNYDKKKLLTHQGESIENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
IDHSGGYVAQFNISWDEVSYDENGNEIKVHKKWGENYKSKLAHFTSSIYLPGNARNINIY 481
                                                                                                                                                                                                                                            QVYVKLSSSSHSNKVKTAFEAAMSGKSVKGDVELTNIIKNSSFKAVIYGGSAKEEVEIID
                                                                                                                                                                                                                                                                                                                                                                     DGKVQEEVISFKQIYYNINVNEPTSPSKFFGGSVTKEQLDALGVNAENPPAYISSVAYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG
                                                       GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                 GNLGELRDILKKGSTYDRENPGVPISYTTNFLKDNDLAVVKNNSEYIETTSKSYTDGKIN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                     AVNDLLAKWHODYGOVN-NVPARXQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
                                                                                                                                                                                  QVYLKLETTSKSxEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                                                                                                                                                                                             SGEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198;
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530 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.5%;
ilarity 42.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THIOL_CYTOLYSINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         530 SE
485 BI
59181 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1476; DB 1;
Pred. No. 5.56e-286;
111; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING TO CHOLESTEROL (BY SIMILARITY).; 68A497A5 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530 AA
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                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                     Matches
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(IN) RAPPUOLI R., ALOUF J.E., FALMAGNE P. (EDS.);
BACTERIAL PROTEIN TOXINS, PP.49-50, GUSTAV FISHER VERLAG,
STUTTGART (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACY_PAEAL P23564;
                                                                                                                                                                                                                              ACT_SITE
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEOFFROY C., MENGAUD J., ALOUF J.E., COSSART P.;
"Alveolysin, the thiol-activated toxin of Bacillus alvei, is homologous to listeriolysin O, perfringolysin O, pneumolysin streptolysin O and contains a single cysteine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAENIBACILLUS ALVEI (BACILLUS ALVEI).
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 91072294.
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15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALVEOLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1991
                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00481; THIOL_CYTOLYSINS; PFAM; PF01289; Thiol_cytolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                EMBL; M62709; G142473; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAENIBACILLUS
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                                                                                                                                                                                                                                                                                                        TOXIN; HEMOLYSIS; CYTOLYSIS;
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                 163
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                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS EUKARYOTIC CELL MEMBRANES.
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                                                                                                                                                                                                                                                                                                                                                                   A37858; A37858
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LVSTWGEKYSSTHTLPARLQYAESMYYSQNQISSALNVNAKYLNGTLGIDFNAVANGEKK 222
                                             LYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRGAVND
                                                                          TYPGAIQLANKDFADNQPSLVMAARKPLDISIDLPGLKNENT-ISVQNPNYGTVSSAIDQ 162
                                                                                                       ILAMNYDKKKLLTHQGESIENRFXKEGNQLPDEFVVXERKKRSLSTNTSDIXVTATNDSR 69
                                                                                                                                     IAGLNYNRNEVLAIQGDQISSFVPKEGIQSNGKFIVVERDKKSLTTSPVDISIVDSITNR 103
                                                                                                                                                                                                                                                                                                                         P19995; 1PFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (REL. 20, CREATED)
1 (REL. 20, LAST SEQUENCE UPDATE)
8 (REL. 37, LAST ANNOTATION UPDAT
PRECURSOR (THIOL-ACTIVATED CYTOL
                                                                                                                                                                                                                               501 AA;
                                                                                                                                                                                                                                             461
56
                                                                                                                                                                  45.3%;
llarity 41.9%;
Conservative
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55268
                                                                                                                                                                                                                                 WW.
                                                                                                                                                                Score 1468; DB 1;
Pred. No. 3.32e-284;
121; Mismatches 141;
                                                                                                                                                                                                                            BINDING TO CHOLESTEROL (BY A -> L (IN REF. 2).
; 8DF2C94A CRC32;
                                                                                                                                                                                                                                                                                                         SIGNAL.
                                                                                                                                                                                                                                                                          POTENTIAL.
ALVEOLYSIN.
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Best Local :
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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PLASMID PMK157.
PIASMID PMK157.
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01-FEB-1991 (REL. 17, LAS
15-JUL-1998 (REL. 36, LAS
STREPTOLYSIN O PRECURSOR
                                                                                                                                                                                                                            TOXIN; HEMOLYSIS; CYTOLYSIS; SIGNAL 1 33
                                                                                                                                                                                                                                                                              PFAM; PF01289; Thiol_cytolysin; HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEHOE M.A., MILLER L., WALKER J.A., BOULNOIS G.J.;
"Nucleotide sequence of the streptolysin O (SLO) gene:
homologies between SLO and other membrane-damaging, thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 88057628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREPTOCOCCUS PYOGENES
                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
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INFECT. IMMUN.
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                                                                                                                                                                                                                                                                                                                                PROSITE; PS00481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.

SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYVAQFEVYWDEFSYDADGQEIVTRKSWDGNWRDRSAHFSTEIPLPPNAKNIRIFARECT
                                                                                                                                                                                                                                                                                                                                                           A43507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLLDHSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VMVAAYKQIFYTVSAGLPNNPSDLFDDSVTFAELARKGVSNEAPPLMVSNVAYGRTIYVK
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                                                                                                                                                                                                                                                                                                                                                                                M18638; G153811;
                                               192;
                                                                       Similarity
                                                                                                                                               34
530
571 AA;
                                                                                                                                                                                                                                                                                                                                                        A43507
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55:3228-3232(1987).
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                                                                                                                                                                                                                                                                                                                              THIOL_CYTOLYSINS;
                                                                       43.7%;
                                                                                                                                                                         571
530
                                                                                                                                                 63638 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rmatics Institute. There are no rest institutions as long as its content
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LAST SEQUENCE UPDATE)

LAST ANNOTATION UPDAT
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(THIOL-ACTIVATED CYT
                                               104;
                                                                    Score 1415; DB 1;
Pred. No. 1.91e-272;
                                                                                                                                                                         STREPTOLYSIN O. BINDING TO CHOI
                                                                                                                                                                                                                                                      SIGNAL; PLASMID.
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                                                                                                                                                 33124E54 CRC32;
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                                               Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      571 AA
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                                                                                                                                                                            CHOLESTEROL
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                                                                                            Length 571;
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                                               Indels
                                                                                                                                                                            (BY SIMILARITY).
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Q54114;
15-JUL-1998
                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95102113.
OKUMURA K., HARA A.,
IGARASHI H., YUTSUDO
                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                    HSSP;
                                                                                                                                                    PROSITE; PS00481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G streptococc:
                                                            TOXIN; HEMOLYSIS; CYTOLYSIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREPTOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Cloning and sequencing the streptolysin O genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           426
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FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
                                                                                                                                                                                                                                                                                                                           by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTIC CELL MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RECTGLAWEWWRKVIDERDVKLSKEINVNISGSTLSP 564
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                                                                                              PF01289; Thiol_cytolysin; P19995; 1PFO.
                                                                                                                                                                                   D16824; G498301;
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                                                                                                                                                    THIOL_CYTOLYSINS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANAKA T., NICHIGUCHI I., MINAMIDE W., T.;
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15-JUL-1998
15-JUL-1998
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Q53957;
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               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                          use
                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
STREPTOLYSIN O PRECURSOR (THIOL-ACTIVATED CYT
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 95102113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 VTDRTYPAALQLANKGFTENKPDAVVTKRNPQKIHIDLPGMGDKAT-VEVNDPTYANVST 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 INDKIYSLNYNELEVLAKNGETIENFVPKEGVKKADKFIVIERKKKNINTTPVDISIIDS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 VFVKLETSSKSNDVEAAFSAALKGTDVKTNGKYSDILENSSFTAVVLGGDAAEHNKVVTK 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 AIDNLYNOWHDNYSGGNTLPARTQYTESMYYSKSQIEAALNYNSKILDGTLGIDFKSISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
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                                                                                                                                                                                                  SEO. 4:325-328(1994).
FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
                                                                                                                                                                EUKARYOTIC CELL MEMBRANES.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEKKVMIAAYKQIFYTVSANLPNNPADVFDKSVTLKELQRKGVSNEAPPLFVSNVAYGRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECTGLAWEWWRKVIDERDVKLSKEINVNISGSTLSP 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHOGAYVAQYEILWDEINYDDKGKEVITKRRWDNNWYSKTSPFSTVIPLGANSRNIRIMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 43.7%; Score 1416; DB 1; Similarity 41.8%; Pred. No. 1.14e-272; 191; Conservative 106; Mismatches 159;
                                                                        non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                        FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533
574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 36, CREATED)
(REL. 36, LAST SEQ
(REL. 36, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 I
63991 MW;
                                                                          institutions as long
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the Euro
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SIGNAL
1 36 BY SIMILARITY.
CHALN
37 574 STREPTOLYSIN O.
ACT.SITE 533 53
BINDING TO CHOLESTEROL
SEQUENCE 574 AA; 63910 MW; 98BD1743 CRC32;
                                                                                                                                                                                                                                                                                                                                          TACY_BACCE
Q45105;
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HSSP; P19995; 1PF0
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                                             This
                                                                                                                                                              SUBMITTED
                                                                                                                                                                                           STRAIN=RIMD 206001;
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                     BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                  BACILLUS CEREUS
                                                                                                                                                                                                                                                                                HEMOLYSIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                              15-JUL-1998 (REL.
15-JUL-1998 (REL.
15-JUL-1998 (REL.
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 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                    MITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES (BY SIMILARITY).
FUNCTION: HEMOLYTIC ACTIVITY AGAINST RED BLOOD CELL.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 43.2%;
Similarity 41.6%;
                                                                                                                                                                                                          FROM N.A.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                     BACILLUS/CLOSTRIDIUM GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104; Mismatches 162;
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                                                                                                                                                                                                                                                      BOS TAURUS EUKARYOTA;
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                         01-MAY-1991 (REL. 18, CREATED)
01-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)
15-DEC-1996 (REL. 37, LAST ANNOTATION UPDATE)
AMINE OXIDASE [FLAVIN-CONTAINING] A (EC 1.4.3.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed
                                  "The primary structure of bovine monoamine with peptide sequences of bovine monoamine flavoenzymes.":
                                                                                            SEQUENCE FROM N.A.

MEDLINE; 89246344.

POWELL J.F., HSU Y.P.P., WEYLER W.,

ANDRIKOPOULOS K., MALLET J., BREAKEI
                                                                                                                                                                                                                            BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                   P21398;
01-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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HSSP; P19995; 1
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Similarity 39.8%; Pred. No. 5.99e-255;
173; Conservative 117; Mismatches 144;
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Best Local
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01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
MITOCHONDRIAL PROCESSING PEPTIDASE BETA SUBUNIT PRECURSOR
(EC 3.4.24.64) (BETA-MPP) (PEP).
MAS1 OR MIF1 OR YIR163C OR L9632.10.
                                                                                                          "MAS1, a gene essential for yeast mitochondrial assembly, subunit of the mitochondrial processing protease."; EMBO J. 7:1439-1447(1988).
      JOHNSTON M., ANDREWS S.,
                                 STRAIN-S288C
                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                            WITTE C., JENSEN R.E.,
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 88312592.
                                                                                                                                                                                                                                                                                                                               SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                      SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P10507;
01-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPPB_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: MONOMER, HOMO- OR HETERODIMER (CONTAINING TWO SUBUIT SIMILAR SIZE). EACH SUBUNIT CONTAINS A COVALENTLY BOUND FLAN ENZYMATICALLY ACTIVE AS MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL OUTER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: CATALYZES THE OXIDATIVE DEAMINATION OF BIOGENIC AND XENOBIOTIC AMINES AND HAS IMPORTANT FUNCTIONS IN THE METABOLISM OF NEUROACTIVE AND VASOACTIVE AMINES IN THE CENTRAL NERVOUS SYSTEM AND PERIPHERAL TISSUES. MAO-A PREFERENTIALLY OXIDIZES BIOGENIC AMINES SUCH AS 5-HYDROXYTRYPTAMINE (5-HT), NOREPINEPHRINE AND PERIPHEREPHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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X15609; G525; ALT_INIT.
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                                                                                                                                                                                                                                                                                                                                                              FUNGI;
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                                                                                                                                                                                                      YAFFE M.P.,
   BRINKMAN R.,
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Pred. No. 2.24e-03;
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COOPER J.,
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                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
SLAP_BACST
P35825;
01-JUN-1994
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                             METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             METAL
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T., HALLSWORPH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D., JOHNSTON L., LANGSTON Y., LARREILLE P., LE T., MARDIS E., MENEZES S., MILLER N., NHAN M., PAULEY A., PELUS RIFKEN L., RILES L., TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M., WILSON R., WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "TANG M., GELI V., OPPLIGER W.
"The MAS-encoded processing protein of the purified purified precursor protein."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 21-32.
MEDILINE; 91177897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X07649; G3887; -. EMBL; U51921; G1234852; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYDROLASE; METALLOPROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00143; INSULINASE; 1.
                                                                                                                                                    185 KNIKSITRTDLKDYITKNYKGDRMVLAG 212
                                                                                                                                                                                    213 VFQDTVTVEDLKQRGISAERPLVYI-Sx-VA--YGRQVYLKL-ETTSKSxEVEAAFEALI
                                                                                                                                                                                                                   125 ILSDILTKSVLDNSAIERERDVIIRESEEVDKMYDEVVFDHLHEITYKDQPLGRTILGPI 184
                                                                                                                   268 KGVKVAPQTEWKQ-ILDNTEVKAVILGG 294
                                                                                                                                                                                                                                                    154 TAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHSGEKQIQIVNxKQIYYTVSV-DAVKNPGD
                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRESEQUENCES FROM MITOCHONDRIAL PROTEIN PRECURSORS.

CATALYTIC ACTIVITY: RELEASE OF N-TERMINAL TRANSIT PEPTIDES FROM PRECURSOR PROTEINS IMPORTED INTO THE MITOCHONDRION, TYPICALLY WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HETERODIMER OF ALPHA AND BETA SUBUNITS. SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THE MITOCHONDRIAL PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INSULINASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16; ALSO KNOWN AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR: REQUIRES DIVALENT CATIONS FOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARG IN POSITION P2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S00552; S00552.
A38734; A38734.
                                                                                                                                                                                                                                                                                      TAHFLEHLAFK-GTQ-NRSQQGIELEIENI-GSHLNAYTSRENTVYYAKSLQEDIPKAVD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L0001026; MAS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00675; Insulinase;
                                                                                                                                                                                                                                                                                                                         Similarity 34; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GELI V., OPPLIGER W., SUDA K., JAMES P., SCHATZ G., rencoded processing protease of yeast mitochondria. ton of the purified enzyme with signal peptides and
                                                                                                                                                                                                                                                                                                                                                                                             150
462 AA;
                                                                                                                                                                                                                                                                                                                         Conservative
                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           70 Z
73 B
74 Z
150 Z
51083 MW;
                                                                                                                                                                                                                                                                                                                                         3.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>, .</u>
                                                                                                                                                                                                                                                                                                                                                                                                       BETA SUBUNIT.

ZINC (BY SIMILARITY).

BY SIMILARITY.

ZINC (BY SIMILARITY).

ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                        Pred.
44; 1
                                                                                                                                                                                                                                                                                                                                         Score 114; DB 1;
Pred. No. 5.17e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZINC; MITOCHONDRION; TRANSIT PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRIAL PROCESSING
                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                             438D1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROCESSING PROTEASE CLEAVES
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                 1228 AA
                                                                                                                                                                                                                                                                                                                                                                                             CRC32;
                                                                                                                                                                                                                                                                                                                                                         Length 462;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELUSO D.,
                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                      212
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(REL. 29, CREATED)
(REL. 29, LAST SEQUENCE UPDATE)

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RESULTATION OF THE SOLUTION OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOP5_YEAST
Q12499;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                    NOP5 OR YOR310C OR 06108.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  surface-layer protein of Bacillus stearothermophilus strain PV72."; GENE 145:115-120(1994).
-!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA;
BACILLUS.
                                                                                                                                     STRAIN=S288C / FY1679;
PEARSON B.M., HERNANDO Y., WOLF S.S., KALA
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQ
15-DEC-1998 (REL. 37, LAST ANN
NUCLEOLAR PROTEIN NOP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X71092; G312730; -. PIR; S34365; S34365. HSSP; P02766; 1ETB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SBSA
                            MEDLINE;
                                                         STRAIN-W30
                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                   SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL; CELL WALL; S-LAYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KUEN B., SLEYTR U.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS STEAROTHERMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE).
S-LAYER PROTEIN PRECURSOR (SURFACE LAYER PROTEIN).
                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the sbsA gene encoding the 130-kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314 NIPFALNTADVSLSTDGKTITVDASTPFENNTEYKVVVKGIKDKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 YDITV-AMKAR-EV-QDAVKAGNLDKAKAAVDQINQYLPKVTDAFKTELT-EVAKKALDA 255
     ۳,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIA IS COVERED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-RFTADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAALTPKVESVS-AINTQNKAVELTAVPVNGT-LKLQLSAAANEDTVNVNTVRIYKVDG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxVAYGRQVYLKLETTSKSxEV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EAAFEALIKGVKVAPQTEWKQI-LDNTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEG 317
BROCKENBROUGH J.S., METCALFE A.C., CHEN S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%;
Similarity 24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                     98298165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94320770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1228 S-I
A; 131076 MW;
                                                                                      AND
                                                                                                                                                                                                                                                                                   SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                        LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUBITZ W.;
                                                                                 CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 114; DB 1;
Pred. No. 5.17e-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
S-LAYER PROTEIN
                                                                                                                                                                                                                                                                                                          HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0D0FB37F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   511 AA
                                                                                                                                                                  KALOGEROPOULOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1228;
                                                                                                                                           BANKS
                                                                                                                                                                                                                                                                                                          SACCHAROMYCETALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 10;
  ARIS J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359
                                                                                                                                                                  Α.,
                                                                                                                                                                     SCHWEIZER M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
                                                                                                                                                          LEE C.Y., MEIGHEN E.A.;

"The lux genes in Photobacterium leiognathi are closely linked with genes corresponding in sequence to riboflavin synthesis genes.";

BIOCHEM. BIOPHYS. RES. COMMUN. 186:690-697(1992).

-!- CATALYTIC ACTIVITY: GTP + 3 H(2)O = FORMATE + 2,5-DIAMINO-6-HYDROXY-4-(5-PHOSPHORIBOSYLAMINO)PYRIMIDINE + PYROPHOSPHATE.

-!- PATHMAY: RIBOFLAVIN BIOSYNTHESIS.

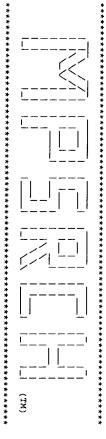
-!- STMILARITY: TO OTHER BACTERIAL GTP CYCLOHYDROLASE II (RIBA), AND TO E.COLI RIBB AND V.HARVEYI LUXH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
GTP CYCLOHYDROLASE II (EC 3.5.4.25) / 3,4-DIHYDROXY-2-BUTANONE 4-PHOSPHATE SYNTHASE (DHBP SYNTHASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCH2_PHOLE
Q02008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X90565; G940841; -. EMBL; Z75217; E252143; -. EMBL; AF056070; G3170533; -. SGD; L0004000; NOP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: REQUIRED FOR PRE-18S RANA PROCESSING.
-1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLUS.
-1- SIMILARITY: BELONGS TO THE NOP5/NOP56 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nop5p is a small nucleolar ribonucleoprotein component required pre-18S rRNA processing in yeast.";
J. BIOL. CHEM. 273:16453-16463(1998).
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 25521;
MEDLINE; 92360014.
                                                                                                                                                                                                                                                                                                                                                                                                                                             BACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR PROTEIN; RRNA PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOTOBACTERIUM LEIOGNATHI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGDLL-LDHSGAYVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGRQVYLKLETTSKSXEVEAAFEALIKGVKV-APQTEWKQIL-DNTEVKAVILGGDPSSG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSLISLAKSPASTIQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEITQTDLDNINALAEQIVEFAAYREQLS-NYLSARMKAIAPNLTQLVGELVGARLIA-H 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASP/GLU/LYS-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F0A4F72C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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DR
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SQ
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Best Local Similarity 20.3%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                               EMBL; M90094; G150708; -.
PFAM; PF00925; GTP_cyclohydro2; 1.
PFAM; PF00926; DHBP_Synthase; 1.
MULTITUNCTIONAL ENZYME; RIBOFLAVIN BIOSYNTHESIS; HYDROLASE.
SEQUENCE 364 AA; 39947 MW; BCE7130C CRC32;
191 TIADLIEYRTQQESHIERISEYELNTEYGI-FTLVTYRDTID-NQAHFALCKGEIQAKAA 248

: : | | | ; | :| : | | | | : | :| 14

140 QVNN-VPARXQYEKITAHSME-QLKVKFGSDFEKTGNSLDIDFNSVHSGEKQIQIVNXKQ 197
                                                                                                                                                                                                       198 IYYTVSV-DAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVAYGRQVYLKLETTSKS 256
                                                                                       249 TLVRVHVKDTLKDILQVGLSQWSLEAAMQRIQTEDGVLVIISQQESPKTLFEKLDMYAK- 307
                                                                                                                                                                                                                                                                         Score 104; DB 1; Length 364;
Pred. No. 9.87e-01;
64; Mismatches 112; Indels 12; Gaps 10;
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Search completed: Mon Aug 30 15:59:26 1999 Job time: 43 secs.



MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 30 15:59:45 1999; MasPar time 29.02 Seconds 885.876 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-120-044-3-COPY (1-471) from devil20044.pep 3241

Sequence: 1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb19
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 49.380; Variance 93.387; scale 0.529

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Resul.
113 113 114 117 118 118	∞ ~ ⊢	ult No.
124 1118 1117 1113 1113 1113 1111 1111 1111	1779 1774 1702	Score
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LISTERIOLYSIN O (FRAGM LISTERIOLYSIN O (FRAGM HYPOTHETICAL 49.7 KD P CHROMOSOME XII READING S-LAYER PROTEIN. S-LAYER PROTEIN. S-LAYER PROTEIN. 187AA LONG HYPOTHETICA HYPOTHETICAL 91.9 KD P HYPOTHETICAL PROTEIN M CHROMOSOME XV READING CONSERVED HYPOTHETICAL PROTEIN B. FROLING-RICH PROTEIN G. CHROMOSOME XV CREADING CONSERVED HYPOTHETICAL PROTEIN B. PROLING-RICH PROTEIN G. CHROMOSOME TV COSMID 9 FLAGELLAR HOOK ASSOCIA HYPOTHETICAL 74.1 KD P CLPB CHAPERONE HOMOLOG	SUILYSIN. HEMOLYSIN. DYOLYSIN	Description
1.79e-03 1.27e-02 1.27e-02 1.27e-02 8.43e-02 6.18e-02 1.15e-01 1.15e-01 1.15e-01 1.25e-01 5.25e-01 5.25e-01 3.89e-01 3.89e-01 1.27e+00 7.07e-01	0.00e+00 0.00e+00	Pred. No.

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	H05L14.2 PROTEIN.	C45G7.6 PROTEIN.	T16B24.10 PROTEIN.	HYPOTHETICAL 97.4 KD P	NIT.	FLAGELLIN (PHASE-1-I F	FISSION YEAST.	D	RESTRICTION ENDONUCLEA	HYPOTHETICAL 155.3 KD	F28B3.7 PROTEIN.	CATION EFFLUX SYSTEM P	ORF910.	HYPOTHETICAL 99.2 KD P	HYPOTHETICAL 96.2 KD P	F32B6.2 PROTEIN.	HYPOTHETICAL 76.5 KD P	FLAGELLIN.	SPORULATION PROTEIN.	PUTATIVE L-AMINO ACID	AMINOTRANSFERASE.	PHOSPHATE TRANSPORT AT	CELL DIVISION INHIBITO	KERATIN 14 (FRAGMENT).
7.08e+00	7.08e+00	7.08e+00	7.08e+00	·	5.35e+00	5.35e+00			5.35e+00	4.03e+00	4.03e+00	1.71e+00		3.03e+00	3.03e+00	3.03e+00	3.03e+00	2.28e+00	4.03e+00		N	1.71e+00	2.28e+00	3.03e+00

ALIGNMENTS

Фр	Db	Оу	Фр	Oy Db	Ma Bo	RR		RESULT
269 SYGRSMFIKLETSSRSTQVQAAFKAAIKGVDISGNAEYQDILKNTSFSAYIFGGDAGSAA 328 	209 DAVNSGEKQVQIVNFKQIYYTVSVDEPESPSKLFAEGTTVEDLKRNGITDEVPPVYVSSV 268 :: : :	149 TVRTGVNNLLSKWNNTYAGEYGNTQAELQYDETMAYSMSQLKTKFGTSFEKIAVPLDINF 208 	89 VIDAKAANIYPGALLRADONLLDNNPTLISIARGDLTLSLNLPGLANGDSHTVVNSPTRS 148 : : :	29 SKODINQYFQSLTYEPQEILTNEGEYIDNPPATTGMLENGRFVVLRREKKNITNNSADIA 88 :: : ::: : : :	Query Match 54.9%; Score 1779; DB 2; Length 497; Best Local Similarity 49.8%; Pred. No. 0.00e+00; Matches 233; Conservative 110; Mismatches 123; Indels 2; Gaps 2;	SEQUENCE OF 1-71 FROM N.A. STRAIN-P1/7; STRAIN-P1/7; STRAIN-P1/7; SEGERS R.P.A.M., KENTER T., DE HAAN W.A.M., JACOBS A.A.C.; "Characterization of the gene encoding suilysin from Streptococcus suis, and expression in field strains."; SUBMITTED (CCT-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; 236907; E1334304; EMBL; 236907; E1334304; SEQUENCE 497 AA; 54850 MW; D78AEBEF CRC32;	: Q55997; 1996 (TREMBLREL: 01, CREATED) 1999 (TREMBLREL: 09, LAST SEQU 1999 (TREMBLREL: 09, LAST ANNO 1990 (TREMBLREL: 09, LAST ANNO 1990 (IN: 1990 (TREMBLREL: 09, LAST ANNO 1990 (IN: 19	LT 1 O55996 PRELIMINARY: PRT: 497 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Streptococcus suis type 2 hemolysin (suilysin) gene. SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AF045356; G3309561; -. SEQUENCE 497 AA; 54778 MW; 36DAB184 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREPTOCOCCUS SUIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OKWUMABUA O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AYGRQVYLKLETTSKGXEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGA
                                                                                                                                                                      LHVNIQECTGLAWEWWRTYYDK-DLPLVGQRKITIWGTTLYPQYADEV
                                                                                                                                                                                                                                                      GDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAVNSGEKQVQIVNFKQIYYTVSVDEPESPSKLFAEGTTVEDLKRNGITDEVPPVYVSSV 268
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                                                                                                                                           LSVKIRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKV
                                                                                                                                                                                                                                                                                             SALTLDHSGAYVAKYNITWEEVSYNEAGEEVWEPKAWDKNGVNLTSHWSETIQIPGNARN 448
                                                                                                                                                                                                                                                                                                                                                                       RVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRN
                                                                                                                                                                                                                                                                                                                                                                                                                             TVVSGNIETLKKIIEEGARYGKLNPGVPISYSTNFVKDNRPAQILSNSEYIETTSTVHNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKQDINQYFQSLTYGPQEILTNEGEYIDNPPATTGMLENGRFVVLRREKKNITNNSADIA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHVNIQECTGLAWEWWRTVYDK-DLPLVGQRKITIWGTTLYPQYADEV 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVVSGNIETLKKIIEEGARYGKLNPGVPISYSTNFVKDNRPAQILSNSEYIETTSTVHNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYGRSMFIKLETSSRSTQVQAAFKAAIKGVDISGNAEYQDILKNTSFSAYIFGGDAGSAA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VTATNDSRLYPGALLVVDETLXENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANKAVNDFILAMNYDKKKLLTHQGESIENRFxKEGNQLPDEFVVxERKKRSLSTNTSDIx 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SALTLDHSGAYVAKYNITWEEVSYNEAGEEVWEPKAWDKNGVNLTSHWSETIQIPGNARN 448
                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98,8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1774; DB 2; L
Pred. No. 0.00e+00;
109; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                          PRT;
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Best Local
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                                                                                                                                                                                                                                                Q48772 PRELIMINARY; PRT; 50 AA.
Q48772;
Q18772;
Q18772;
Q18772;
Q18772;
Q18772;
Q18772;
Q1 CREMBLREL 01, CREATED)
Q1 NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
Q1 NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
LISTERIOLYSIN O (FRAGMENT).
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01-JAN-1998
01-NOV-1998
                           SEQUENCE FROM N.A. STRAIN=11984, TYPE 1; MEDLINE; 96118685.
                                                                                                                                                                          LISTERIA MONOCYTOGENES BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BILLINGTON S.J., JOST B.H., CUEVAS W.A., BRIGHT K.R., S "The Arcanobacterium (Actinomyces) pyogenes hemolysin, novel member of the thiol-activated cytolysin family.", D. BACTERIOL. 179:6100-6106(1997).

EMBL; U84782; G2252800; -.

PFAM, PF01289; Thiol_cytolysin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARCANOBACTERIUM PYOGENES.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; ACTINOMYCINEAB; ACTINOMYCETACEAE; ARCANOBACTERIUM.
RASMUSSEN O.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRNLSVKIRECTGLAWE-WWRTYYEKTDLPLYRKRTISIWGTTLYPQVEDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARNIHVEAGEATGLAWDPWW-TVINKKNLPLVPHREIVLKGTTLNPWVEDNV 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKSGEITFRHGGGYVAKFRLKWDEISYDPQGKEIRTPKTWSGNWAARTLGFRETIQLPAN 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIHKRERQVAIASFKQIYYTASVDTPTSPHSVFGPNVTAQDLKDRGVNNKNPLGYISSVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGRQVYLKLETTSKSXEVEAAFEALIKG--VKVAPQ--TEWKQILDNTEVKAVILGGDPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVHSGEKQIQIVNxKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISXVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGVEVATGNIDALKKIIKEESTYSTKVPAVPVSYAVNFLKDNQLAAVRSSGDYIETTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFDANNAHVYPGALVLANKDLAKGSPTSIGIARAPQTVSVDLPGLVDGKNKVVINNPTKS
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(TREMBLREL. 05, LAST SEQUENCE UPDATE)
(TREMBLREL. 08, LAST ANNOTATION UPDATE)
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larity 40.0%;
Conservative
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AA; 57873 MW; I
SKOUBOE
                                                                                                                                                                          BACILLUS/CLOSTRIDIUM
٩.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1302; DB 2; Length 53
Pred. No. 1.55e-248;
121; Mismatches 154; Indels
DONS
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L.,
ROSSEN L.,
                                                                                                                                                                             GROUP;
OLSEN
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J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SONGER J.G.;
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FIGURE SULP PROBLEM SULP PROBLE
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Best Local Similarity
""" Conserv
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Best Local
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Q48773;
                                                  MEDLINE; 96347136.
MEDLINE; 96347136.
TRUDEAU K.G., WARD M.J., ZUSMAN D.R.;
"Identification and characterization regulator necessary for swarming and
                                                                                                                                                                                                                                                                  01-AUG-1998 (TREMBLREL 07, CI
01-AUG-1998 (TREMBLREL 07, LI
01-NOV-1998 (TREMBLREL 08, LI
HYPOTHETICAL 49.7 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
NON_TER
                                                                                                                                                                                                   BACTERIA; PROTEOBACTERIA; DELTA SUBDIVISION; MYXOBACTERIA; MYXOCOCCALES; CYSTOBACTERINEAE; MYXOCOCCACEAE; MYXOCOCCUS.
                                                                                                                                                                                                                                                   MYXOCOCCUS XANTHUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Listeria monocytogenes exists in evidence from flagellin, invasive listeriolysin O genes", MICROBIOLOGY 141:2053-2061(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Listeria monocytogenes exists in at least three evolution evidence from flagelin, invasive associated protein and listeriolysin O genes."
MICROBIOLOGY 141:2053-2061(1995).
                                       Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RASMUSSEN O.F., SKOUBOE P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=206.1.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISTERIA MONOCYTOGENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284
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Local Similarity 34.7%;
les 17; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 NSSFKAVIYGGFAKDEVQIIDGNLGDLRDILKKGATFNRETPGVPIAYT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NSSFKAVIYGGSAKDQVQIIDGNLGDLRDILKKGATFNRETPGVPIAYT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYT 332
                     MICROBIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X85935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X85855; G940601; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96118685
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larity 34.7%;
Conservative
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                   20:645-655(1996)
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                                                                                                                                                                                                                                                                                    07, CREATED)
07, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 118;
Pred. No. 1.
14; Mismatc
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sts in at least three evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 124; DB 2;
Pred. No. 1.79e-03;
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d. No. 1.27e-02;
Mismatches 18;
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ANNOTATION UPDATE)
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                                                  of Frzz, a novel response fruiting-body formation in
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Q12098;
Q12098;
Q1-NOV-1996 (TREMBLREL. 01, ....
T 01-NOV-1996 (TREMBLREL. 01, LAS)
DE CHROMOSOME XII READING FRAME OF
19606 6 OR L3140.
***CFS CEREVISIAE (BAK)
***COMYCOTA;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                        STRAIN-S288C (AB972);
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T.,
HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,
MILLER N., NHAN M., PAULEY A., PEUUSO D., RIFKEN L., RILES L.,
TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.
MILSON R., WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WARD M.J., ZUSMAN D.R.;
SUBMITTED (FEB-1998) TO EM
SUBMIT AF049107; G2947295;
EMBL; AF049107; G2947295;
HYPOTHETICAL PROTEIN.
                                     SUBMITTED (SEP-1995) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; 273307; E245572; -. EMBL; 2556901; -. EMBL; X91258; G995701; -. EMBL; X91258; G995701; -. SEQUENCE 748 AA; 84361 MW; 4900A1F6 CRC32;
                                                                                                                                                                             WATERSTON
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (MAY-1996) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L9606.6 OR L3140.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
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                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                 SUBMITTED (APR-1996)
                                                                                                                                                                                          STRAIN-S288C (AB972);
                                                                                                                                                                                                                                     SUBMITTED
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                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288C (AB972);
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 PLVYI-SXVAYGRQVYLKLETTSKSXEVEAAFEALIKGVKVAPQTEWKQI-LDNTEVKAV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 ILGGDPSSGARVVTGKVDMVEDLIQEGSRFTADHPG--LPISYTTSFLRDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 HLPGRLPVGLHPETGELELVREMKVGGKTFVPNAVGALLPPGYTRTFLPGEV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 3.6%;
Local Similarity 26.8%;
hes 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 PLVLVTSDMTFAPKL-LFADPKGRVMEHPYLLATLRSGEELVPPQD-KPIPLPSTG-RLV 65
                                                                                                             Η.
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                                                                                                                                                                                                                                    (APR-1996) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAY-1996) TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               450 AA;
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3.5%;
18.8%;
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01, LAST SEQUENCE UPDATE)
01, LAST ANNOTATION UPDATE)
FRAME ORF YLR135W.
                                                                                                                                                                 EMBL/GENBANK/DDBJ DATA BANKS
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Score
Pred.
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27; M
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Pred. No. 1.75e-02
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112;
No. 8.
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DB 3;
1.43e-02;
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Best Local S
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087083;
01-NOV-1998
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                    030524;
01-JAN-1998
01-TAN-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  determination and function of the recombinant protein."; FEMS MICROBIOL. LETT. 166:275-281(1998). EMBL; AB001876; D1034498; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAMPYLOBACTER RECTUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAMPYLOBACTER.
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                                      SEQUENCE FROM N.A
                                                                                                                CAMPYLOBACTER
                                                                                                                                                       BACTERIA;
                                                                                                                                                                                       CAMPYLOBACTER RECTUS
                                                                                                                                                                                                                                                                 S-LAYER PROTEIN.
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Local Similarity 21.0%;
hes 39; Conservation
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                                                                                                                                                PROTEOBACTERIA;
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8 (TREMBLREL.
6 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
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LAST SEQUENCE ANNOTED
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Pred. No. 6.18e-02;
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                                                                                                                                                SUBDIVISION; CAMPYLOBACTER GROUP;
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WANG B., KRAIG E., KOLODRUBETZ D.;

"A new member of the S-layer protein family: characterization of the crs gene from Campylobacter rectus.";

INFECT. IMMUN. 66:1521-1526(1998).

EMBL; AFOLO143; G2459961;

EMBL; AFOLO143; G2459961;

SEQUENCE 1361 AA; 144385 MW; CAFE081F CRC32;
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01-AUG-1998 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                        HYPOTHETICAL T5K18.220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete Sequence and Gene Organization of the Hyper-thermophilic Archaebacterium, Pyrococcus h DNA RES. 5:55-76(1998).
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MEDLINE; 98344137.
MEDLINE; 98344137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174
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                                                                                                                                                                                                                                                                                     234 LVYISXVAYGRQVYLKLETTSKSXEVEAAFE-ALIKGVKVAPQTEWKQILDNTEVKAVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP000002; D10
NCE 187 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 3.5%;
Similarity 21.0%;
39; Conservative
                                              (TREMBLREL. ()
(TREMBLREL. ()
(TREMBLREL. ()
1 (TREMBLREL. ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D1030351;
                                                                                                                                                                                                                                                                                                                                                                                                                  3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21959 MW;
                                              PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07, CREATED)
07, LAST SEQUENCE OF LAST ANNO
                                                                      07, CREATED)
07, LAST SEQUENCE UF
07, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THERMOCOCCALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 113; DB 2;
Pred. No. 6.18e-02
49; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                               Score 111; DB 1;
Pred. No. 1.15e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8EC990E3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                             814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THERMOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                ₿
                                                                                                    UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 187,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y., SHIZUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                            6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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ARABIDOPSIS THALIANA (MOUSE-EAR CRESS)

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RESULT OLD COMMENS OF SOME FIRST 
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Best Local Similarity 26.3%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998
01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jannaschii.";
SCIENCE 273:1058-1073(1996).
-I- SIMILARITY: STRONG, TO A.FULGIDUS AF1550 AND
M.THERWOAUTOTROPHICUM MTH576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE; 96337999.

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

KERLAYAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,

OVERBEEK R., KIRKNESS E.F., WEIMSTOCK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus

Jannaschil.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67570; G1591933; -. HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARCHAEA; EURYARCHAEOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHANOCOCCUS JANNASCHII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q58691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU ARABIDOPSIS SEQUENCING PROJECT;
SUBMITTED (APR-1998) TO EMBL/GENBA
EMBL; AL022580; E1287635; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHANOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BEVAN M., VAN DER SCHUEREN J., CHUANG Y-J., VOET M.,
VOLCKAERT G., BANCROFT I., MEWES H.W., MAYER K.F.X.,
SUBMITTED (APR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                127
                                                                                                                                                                 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAPPARALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              729 EMHSKNYHPNKITYTVMIGGYARDGNVTEASRLLNEMREKGIVPD-SITYKEFIYGYLKO 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 VYLKLETTSKSXEVEAAFEALIKG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 788 GGV-LEA-FKGSD-EENYAAIIEG 808
                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 3.4%;
Local Similarity 23.8%;
Conservative
V-FQDTVTVEDLKQRGISAE 231
                                                                    PGFIDKETAENLKENDIFVE 146
                                                                                                                                            ITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHSGEKQIQIVNxKQIYYTVSVDAVKNPGD 212
                                                                                                                                                                                                                    IVGVELTHIPPKSIPKMAKKAKDLGAEIVVVH-GETVVEPVEEKTNYYASISEDVDILAH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKQIQIVNXKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISxV-AYGRQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TREMBLREL.) (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  814 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24666 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REL. 06, REL. 06, NEL. 06, NEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91943 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHANOCOCCALES; METHANOCOCCACEAE;
                                                                                                                                                                                                                                                                                                              Score 107; DB 1;
Pred. No. 3.89e-01;
17; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 111; DB 10;
Pred. No. 1.15e-01;
29; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CFC99AB9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A41B8987 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 AA.
                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                           Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 814;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHUELLER
                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ن</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ი
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RESULT 13

OLIZO44;
AC Q12044;
AC Q12044;
AC Q12044;
AC Q12044;
DT O1-NOV-1996 (TREMBLREL. O1, CREATED)
DT O1-NOV-1996 (TREMBLEEL O1, LAST SEQUENCE UPDATE)
DT O1-NOV-1996 (TREMBLEEL O1, LAST SEQUENCE UPDATE)
DT O1-NOV-1996 (TREMBLEEL O1, LAST ANNOTATION UPDATE)
DE CHROMOSOME XV READING FERAME ORF YOR220W.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC SACCHAROMYCETACEAE; FUNGI; ASCOMYCOTA; HEMLASCOMYCETES; SACCHAROMYCETALES;
RN [1]
RP SEQUENCE FROM N.A.
RA BOYER J., FAIRHEAD C., GAILLON L., GALISSON F., MICHAUX G.,
RN [2]
RN SEQUENCE FROM N.A.
RA THIERRY A., DUJON B.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RA GALISSON F., DUJON B.;
RA GALISSON F., DUJON B.;
SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
BR SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RA GALISSON F., DUJON B.;
SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
BR EMBL; X79128; E252085;
DR EMBL; X92441; G1050772;
-
DR EMBL; X92441; G1050772;
-
SQ SEQUENCE 265 AA; 29255 MM; 2D5DD78E CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             028947
028947;
01-JAN-1998
01-JAN-1998
01-AUG-1998
                                                                                                                   KLENK H. P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E., KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D., RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E. KYRPIDES N.C., FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S., KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B., PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU OVERBEEK R., GOCAYME J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T. COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M., SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A., MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                    "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus."; NATURE 390:364-370(1997).
                       EMBL; AE001012; G2649254; TIGR; AF1322; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                      STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE; 98049343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONSERVED HYPOTHETICAL PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 SINKGGSSLSPDKSSLESPTMLKLSTDSKPFSYQEPLPKLSRSSS
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Similarity 26.7%;
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05, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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Pred. No. 5.25e-01;
26; Mismatches 44; Indels
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                                                                                                                                                                                                    UTTERBACK T.,
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Search completed: Mon Aug 30 16:01:04 1999 Job time: 79 secs.
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Best Local Similarity 27.5%;
Matches 22; Conservative
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O85915
PRELIMINARY; PRT; 710 AA.
O85906;
O1-NOV-1998 (TREMBLREL. 08, CREATED)
O1-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
O1-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
TRANSPONSON PROTEIN B.
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ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK E.C.,

SENSEN C.W., GAASTERLAND T., SAFFER J.D., FREDRICKSON J.K.;

"Complete sequence of a 184 kb catabolic plasmid from Sphingomonas
arcumaticivorans strain F199,";

SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AF079317; G3378338; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLASMID PNL1.
BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; ZYMOMONAS GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPHINGOMONAS AROMATICIVORANS.
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                                                                                                                                                                                                                                                                                                                                                                                                                          139 NHHNDAVLECYAAWYGANYGRR-RQSQT-RQWIRGGKIVTSEFRSPEVQLFGDIHRFAII 196
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                                                                                                                                                                                  425 IR 426
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Tabular output not generated. Mon Aug 30 16:08:23 1999; MasPar time 18.55 Seconds 539.888 Million cell updates/sec

>US-09-120-044-3

Description:
Perfect Score:
Sequence:

(1-471) from USO9120044.pep 3299
1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
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34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 35.522; Variance 172.880; scale 0.205

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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W61278 R05079	W55347 W55528	R77673 W22862	R88135 W60976	W60952	R10376	R33841	R33842	R05924	R05923	ID
Monamine oxidase A. Human monoamine oxida	H. pylori ORF 01cell6 H. pylori ORF 29ge303	S-layer protein encod Bacillus stearothermo	Listeriolysin O haemo Streptococcus pneumon	Streptococcus pneumon	Streptolysin O deriva	Soluble streptolysin	Streptolysin O varian	Immunogenic pneumolys	Immunogenic pneumolys	Description
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	121 ssvrgavndllakwhqdygqvnnvparmqyekitahsmeqlkvkfgsdfektgnsldidf 180	61 SVTATNDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSN 120	61 svtatndsrlypgallvvdetllennptllavdrapmtysidlpglassdsflqvedpsn 120	1 MANKAVNDFILAMNYDKKKLLTHQGESIENRFIKEGNQLPDEFVVIERKKRSLSTNTSDI 60	1 mankavndfilamnydkkkllthqqesienrfikeqnqlpdefvvierkkrslstntsdi 60	Query Match 99.9%; Score 3297; DB 1; Length 471; Best Local Similarity 99.8%; Pred. No. 5.72e-275; Matches 470; Conservative 1; Mismatches 0; Indels 0; Gaps	Sequence 471 AA;	making them useful in vaccination against pneumonia and associated	Vaccines are non-toxic and antigenic to wild type pneumolysin,	sequences encoaing them. Claim 5: Page 11: 25pp: English.	nst Streptoco	molysin - useful	•	WALKER JA;	PATON JC, HANSMAN DJ, BOULNOIS GJ, ANDREW PW, MITCHELL TJ,	•		15-JEC-1886. BIID536		s pneumoniae.	Pneumolysin; vaccine; pneumonia; meningitis; bacteriaemia; ds.	Immunogenic preumolysin variant	1000	ET 1 R05923 standard; protein; 471 AA.	

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Best Local
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Vaccines are non-toxic and antigenic to wild type pneumolysin, making them useful in vaccination against pneumonia and associ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 90-224494/29.

New non:toxic, immunogenic mutants of pneumolysin receive vaccines against Streptococcus pneumoni
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15-DEC-1989; AU0539.
16-DEC-1988; AU-001989.
(PATO/) PATON J.C.
PATON JC, HANSMAN DJ, BOULNOIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Pred. No. 2.05e-259;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents a soluble variant of Streptolysin O (SLO) having no haemolytic activity. The variant SLO can specifically recognise wild-type anti-SLO antibodies (ASO) but has no haemolytic activity. It can be used for the determination of previous and/or current infection by Streptococcus pyogenes. It enables ASO assays to become commercially viable and avoids the risk of handling haemolytically active S. pyogenes wild-type SLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptolysin O variants produced by recombinant DNA technology having no haemolytic activity and recognised by wild-type anti-streptolysin O antibodies, useful in diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes infection Claim 17; Fig 2; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus pyogenes; ASO. Streptococcus pyogenes.
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N-PSDB; Q38287.
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30-AUG-1991;
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                                                                                                                                                                                                                                                                                                                                                                   GAVNDLLAKWHQDYGQVNNVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
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US-752428.
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Pred. No. 7.18e-11;
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Matches 19
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Claim 7; Fig 2; 60pp; English.
The sequence is that of a soluble deriv. of Streptolysin O
The sequence is that of a soluble deriv of Streptococcus pyogenes
genomic library clone rSLO.3. It is useful in immunodiagnostic assays
which rely upon, e.g. the haemolytic properties of wild type
Streptolysin O. Recombinant Streptolysin O is obtd. more cheaply
than purified Streptolysin O obtd. from Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deriv. of streptolysin 0 with haemolytic activity immuno-diagnostic assays which rely on haemolytic wild-type Streptolysin 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-JUL-1992; U06398.
30-AUG-1991; US-752429.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soluble streptolysin O variant. Recombinant; haemolytic activity; immunodiagnostic activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1993 (first entry)
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Local Similarity 42.4%;
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      IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP
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                                                                asectglawewwrkviderdvklskeinvnisgstlsp
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                                                                                                                                                                                                                                                                 GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGEKQIQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYGR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAVNDLLAKWHQDYGQVNNVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
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                                                                                                                                    LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
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Pred. No. 2.68e-110;
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Deriv. of thiol-activated protein streptolysin 0 - contg. no cysteine amino acid but retaining cytolytic activity, used detecting antibodies in samples Disclosure; Fig 2; 9pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptolysin O derive*'
SLO.
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04-JAN-1989; GB-000107.
(KEHO/) KEHOE M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The SIO derivative contains no cysteine residues, with cytolytic activity giving resistance to inactivation by oxidation or thiol groups. Abs raised to the SIO may be used in the dection a diagnosis of Streptococcus pyogenes infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kehoe M, Pinkney M;
WPI; 91-024598/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kdfdvirnvikdnatfsrknpaypisytsvflknnkiagvnnrteyvettsteytsgkin
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Similarity 42.4%;
194; Conservative
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No. 1.09e-109;
Mismatches 153;
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22-NOV-1990 (first entry)
Bacteriophage lambda FL promoter - streptolys
protein of plasmid pMX306.
Streptolysin 0; SiO; protease; bacteriophage
Streptococcus pyogenes.

streptolysin O (SLO)

lambda;

cleavage_site

ocation/Qualifiers

R06000 standard; protein; 371

R06000;

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RESULT RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
of meningitis
Claim 11; Page 53; 130pp; English.
The sequence is that of the polypeptide encoded by a region isolated from S. pneumoniae which shows homology to pneumolysin.
The protein, or agonists of it, may be useful as an antibacterial form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-1990.
17-NOV-1989; 026008.
18-NOV-1988; GB-027038.
17-NOV-1989; GB-026008.
(KEHO/) KEHOE M.
                                                                                                                                                                                                                                                                                                                                            14-MAY-1998.
27-OCT-1997; U19226.
201-NOV-1996; US-029930.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                   e.g.
                                                                                                                                                                                                                                                        N-PSDB; V37352.
                                                                                                                                                                                                                                                                                                        Black MT, Hodgson JE,
Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptococcus pneumoniae encoded polypeptide coding region; ORF; open reading frame; antik
                                                                                                                                                                                                                          New isolated nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9819689-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W60952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W60952 standard; Protein; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to streptolysin O.
Disclosure; pp; English.
SLO derivative is epitopic
used in detecting anti-SLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection; prevention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-toxic and non-cytolytic derivs. of streptolysin raising antibodies, purifying antibodies or detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q05240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEHOE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418 VRNLSVKIRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 aanpllvgvsakpvnqwhdnyspgntlpartqytesmvysksqieaalnvnskildgtlg 79
                                                                                                                                                                                                                                                                               98-286586/25.
                                                                                                                                                                                           isolated nucleic acids from Streptococcus pneumoniae for identifying anti-bacterial(s) for treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        srnirimarectglawewwrkviderdvklskeinvnisgstlsp 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ehnkvvtkdfdvirnvikdnatfsrknpaypisytsvflknnkiagvnnrteyvettste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           snvaygrtvfvkletssksndveaafsaalkgtdvktngkysdilenssftavvlggdaa 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSNSSYRGAVNDLLAKWHQDYGQVNNVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDFNSVHSGEKQIQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                idfksiskgekkvmiaaykqifytvsanlpnnpadvfdksvtfkelqrkgvsneapplfv 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YRNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSVAYGRQVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n 33.8%;
Similarity 43.2%;
149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=Lambda N promoter - SLO.
                                                                                                                                                                                                                                                                                                                              Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to its wild type Abs, indicating p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1114; DB 1;
Pred. No. 3.95e-83;
78; Mismatches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 118;
                                                                                                                                                                                                                                                                                                                           Lonetto MA, Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    presence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ptolysin 0 - used for
detecting antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Strepton
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                                                                                                                                                                                     prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
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Š В

427

ECTGLAWEWWR 437

1 ectglawewwr 11

Matches

Mismatches

Indels

0,

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Length 11;

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IN THE SULT THE COLOR OF THE CO
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Example 3; Page 13; 23pp; English.

C The present peptide is a listeriolysin O (LLO) haemolytic domain (HD) fragment, which is 100% conserved in the LLO homologues streptolysin O, and pneumolysin. A 201 bp fragment encoding the LLO Streptolysin O, and pneumolysin. A 201 bp fragment encoding the LLO C cluble molecular complex, for the specific targetting of a polynucleotide (PN) to a cell. The complex comprises a PN, a carrier comprising a PN binding agent and a cell specific binding agent, which binds to a surface mol. of the cell and is internalised into an endosome, and a bacterial component (i.e. the PN into cell's cytoplasm. The complex can be used therapeutically considered the cell's cytoplasm. The complex can be used therapeutically considered the cell's cytoplasm. The complex can be used therapeutically considered the cell and is considered to the cell's cytoplasm. The complex can be used therapeutically considered the considered the cell and considered the cell and considered the cell and considered the cell considered the considered the considered the cell cell's cytoplasm. The complex can be used the cell cell cell's cytoplasm.
                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeriolysin O; haemolytic domain peptide.
Listeriolysin O; haemolytic; domain; streptolysin O; pneumolysi soluble molecular complex; specific; targetted; polynucleotide; endosome lysis; bacterial component; cytoplasm; therapeutic; in vivo; ex vivo; in vitro; delivery; cell specific; hemolytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-1996.
27-JUN-1995; U08091.
29-JUN-1994; US-267710.
07-JUN-1995; US-484009.
                                                                                                                                                       Sequence
                                                                                                                                                                                        specific
                                                                                                                                                                                                              PN into cell's cytoplasm. The complex can be used to enhanced in vivo, ex vivo or in vitro delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IT 8
R88135 standard; peptide;
R88135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble molecular complex for specific targetting of PN to cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carmichael E, Spi
WPI; 96-077502/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TARG-) TARGETECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCO-) UNIV CONNECTICUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 RNLSVKIRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQV-EDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 RNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 rnlrvkiekktgllwnrwqtiyenrpilaqphrkithwgttlnskvsdddv 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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Similarity 100.0%;
11; Conservati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.18;
Similarity 43.28;
                                                                                                                                                                                    cell
                                                                                                                                                       11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spitalny GL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                    Score 112; DB 17;
Pred. No. 6.98e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
32; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wu CH, Wu GY, Zhang Y;
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No. 1.75e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specifically caused by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                  PN to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468
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RESULT RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of the polypeptide encoded by a region isolated from 5. pneumoniae which shows homology to nicotinate-nucleotide pyrophosphorylase. It, or agonists of it, may be useful as an antibacterial for treatment or prevention of infection, specifically caused by 5.pneumoniae (particularly meningitis) but possibly also Helicobacter pylori (ulcers and gastric cancer). It may be of particular use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular
                                                                                                                                                                                                                                                                                                                                                                                             S-layer protein encoded by sbsA gene sbsA gene; S-layer; cell surface lay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 10
R77673 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression. Detecting a sequence encoding the protein can be used diagnostically, e.g. to detect a mutation for serotyping or classifying infectious agents.

Sequence 299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of meningitis
Claim 11; Page 71-72; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g.
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Reid RH, Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1998.
27-OCT-1997; U19226.
01-NOV-1996; US-029930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9819689-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae encoded polypeptide. coding region; ORF; open reading frame; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W60976
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                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                     Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; prevention;
                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1996
                                                       Lubitz W;
                                                                               25-JAN-1996.
19-JUL-1994; 425527.
19-JUL-1994; DE-425527.
(VOGE-) VOGELBUSCH GMBH
                                                                                                                                                                                                 DE4425527-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolated nucleic acids from Streptococcus pneumoniae - useful, for identifying anti-bacterial(s) for treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98-286586/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALLYVDETLLENNPTLLAVDRAPMTYSIDLPGLAS-SDSFLQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gdl-vl-e-iigsvrslltcervalnflqhlsgiasmtaayve 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dystnaifdhhgqakvslfakeagvlag-ltvfqrvftlfdaevtfqnphqfkdgdrlts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NYDKKKLLTHQGESIENRFIKEGNQLPDEFVVIERKKRSLSTNTS-DISVTATNDSRLYP 72
                          96-077933/09
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Similarity 21.4%;
22; Conservati
                                                                                                                                                                                                                                                                                                                                                                        stearothermophilus
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                                                                                                                                                                                                                                                      /label= sig_peptide 31..1228
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitis.
                                                                                                                                                                                                                            mat_proteir
                                                                                                                                                                                                                                                                                                                                                                                                surface Layer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 110; DB 33;
Pred. No. 9.46e+00;
38; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                                                                                                                                                                                expression.
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Query Match
Best Local S
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The claimed signal peptide encoding sequence (see tag e of T0869: is pref. operably linked at the 3' end to a protein encoding sequence. The protein is pref. the S-layer protein (see tag f of T08695), At the 5' end, the signal peptide encoding sequence is pref. linked to an expression control sequence, pref. the sequence given in T08696.
                                                                                  s-layer protein, sbs-A. S-layer structures can be used as vaccines or adjuvants, particularly when they include a bacterial ghost that may contain additional epitopes in its membrane. Other uses of recombinant sbs-A depending on the nature of the inserted peptide, are as an universal carrier for biotinylated reactants for use in immunological or hybridisation assays (the insert is streptavidin), to induce immune responses (epitopes), as a reagent for removing cytokine or toxin from serum (antigenic epitopes), as a molecular spinning nozzle (polyhydroxybutyrate synthase) and as a molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding signal peptide of Bacillus stearothermophilus s-layer protein - which has a lysine content of at least 10 per
                                                                                                                                                                                                                                            recombinant proteins containing heterologous inserts, e.g. epitope(s), useful as vaccines and adjuvants Claim 1; Pages 9-14; 31pp; German.
The present sequence is the Bacillus stearothermophilus PV72
                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                   Preparation of S-layer proteins by expressing sbs-A gene in negative bacterium - or new sbs-B gene in any host, also new
                                                                                                                                                                                                                                                                                                                                                        N-PSDB; T75487
                                                                                                                                                                                                                                                                                                                                                                                                       (LUBI/) LUBITZ W. (SLEY/) SLEYTR U.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996; DE-003649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE19603649-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular spinning nozzle; molecular laser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-layer; sbs-A; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus stearothermophilus S-layer protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                       Kuen B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996; 003649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 S-RFTADHPGLPISYTTSFLRDNVVATFQNSTDY-VETKVTAYRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     314 nipfalntadvslstdgktitvdastpfennteykvvvkgikdkng
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                                                                         .aser (luciferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 yditv-amkar-ev-qdavkagnldkakaavdqinqylpkvtdafktelt-evakkalda 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                        B, Lubitz W,
97-394558/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEAAFEALIKGVKVAPQTEWKQI-LDNTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deaaltpkvesvs-aintqnkaveltavpvngt-lklqlsaaanedtvnvntvriykvdg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYGRQVYLKLETTSKS-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%;
Similarity 24.7%;
41; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stearothermophilus
                                                      1228
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                                                      AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 110; DB 17;
Pred. No. 9.46e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carrier; hybridisation assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence, pref. the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sbs-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1228;
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Matches

Local Similarity hes 41; Conser

Conservative

3.3%;

Score 110; DB 25; Pred. No. 9.46e+00;

Length 1228;

Indels

10;

Gaps

10;

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В
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                                                                                                                     Ъ
                                                                                                                                                                                                                                                                                        PT Helicobacter pylori nucleic acid sequences and encoded
PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori
PT infection and for diagnosis of H. pylori infection
PS Claim 14; Page 571; 1145pp; English.

CC This sequence is a H. pylori protein of unspecified function.

CC This sequence is a H. pylori protein of unspecified function.

CC This sequence is a H. pylori polypeptide binding compounds,

CC infection or to identify H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors. The

CC DNA and probes derived from it may be used for the identification of

CC L. pylori in a sample and the diagnosis of H. pylori infection. Nucleic

CC acid sequences complementary to the DNA act as antisense sequences and

CC argainst the protein can be used in immunoassays to evaluate the abundance

CC and distribution of H. pylori-specific antigens. The genomic sequence of

CC H. pylori (ATCC 55679) was determined from overlapping contigs generated

CC defined by computer evaluation. To identify likely H. pylori antigens for

CC vaccine development, the amino acid sequences predicted coding regions

CC defined by computer evaluation. To identify likely H. pylori antigens for

CC were analysed for significant homology to other known or exported

CC interest, particular regions can be isolated from H. pylori by PCR

amplification for recombinant polypeptide production. English pCR

controlled to the combinant polypeptide production of the sequences of
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                                                                                                                                                              Matches
                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASTR ) ASTRA AB.
Alm RA, Smith D;
WPI; 97-503122/46.
N-PSDB; V24756.
                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W55347 standard; Protein; 188
W55347;
17-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                      amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
02-APR-1996; US-758731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9737044-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori.
270 V 270
                                      152 1 152
                                                                               210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 nipfalntadvslstdgktitvdastpfennteykvvvkgikdkng
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                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pylori ORF 01ce11618orf11 protein.
                                                                                                           psslmrdsvsledskkr-lnaikdlifhknkaf-rqlqlklntplka-lveaqkdgefka 151
                                                                        PGDVFQDTVTVEDLKQRGISAERPLVYISSVAYGRQVYLKLETTSKSDEVEAAFEALIKG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       deaaltpkvesvs-aintqnkaveltavpvngt-lklqlsaaanedtvnvntvriykvdg 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEAAFEALIKGVKVAPQTEWKQI-LDNTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYGRQVYLKLETTSKS-DE 258
                                                                                                                                                              Similarity
21; Conse
                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-738859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-736905
                                                                                                                                                                                                                                                                                for recombinant polypeptide production, e.g. in E.
                                                                                                                                                                                                                                                AA,
                                                                                                                                                                             3.2%;
                                                                                                                                                          Score 104; DB 29;
Pred. No. 2.32e+01;
21; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                          16;
                                                                                                                                                                                              Length 188;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PT Helicobacter pylori nucleic acid sequences and encoded PT polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection PS Claims 14,93; Page 730-731; 1145pp; English.

CC This sequence is a H. pylori cellular protein.

CC This sequence is a H. pylori or polypeptide binding compounds, The protein may be used in a vaccine to prevent or treat H. pylori CC useful as potential H. pylori life cycle activators or inhibitors. The CDNA and probes derived from it may be used for the identification of CC H. pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and CC can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance CC and distribution of H. pylori-specific antigens. The genomic sequence of the pylori (ATCC 55679) was determined from overlapping contigs generated CC membranically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions CC vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported interest, particular regions can be isolated from H. pylori by PCR complification for recombinant polypeptide production, e.g. in E. coli nears.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
3.2%;
Best Local Similarity 34.4%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-1997; U05223.
27-MAR-1997; U05223.
06-DEC-1996; US-761318.
29-MAR-1996; US-625811.
29-APR-1996; US-758731.
30-APR-1996; US-736505.
                                                                                                                                                                                                                                                                 Growth hormone; coho salmon growth hormone; csGH; transgenic; abalone; actin; ACT5-C; insulin-like growth factor; cytochalasin B;
                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1996 (first entry) Coho Salmon growth hormone.
         protein
                                                                                                                                                                                                                                                                                                                                                                                                                          R80623;
12-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R80623 standard; Protein; 210
                                                                                                    peptide
                                                                                                                                                                                          Oncorhynchus keta.
                                                                                                                                                                                                                                         polyploid
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Alm RA, Smith D;
WPI; 97-503122/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; V24937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-1996; US-736905.
28-OCT-1996; US-738859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
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W55528 standard; Protein; 418 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism.
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ORF 29ge30321_24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
/note= "signal peptide"
23..210
                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 104; DB 29;
Pred. No. 2.32e+01;
21; Mismatches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.0%;
Best Local Similarity 25.5%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
US5783680-A.
21-UUL-1998.
26-OCT-1993; 132168.
06-OCT-1993; US-132168.
(GEN HOSPITAL CORP.
(UYKA-) UNIV STICHTING KATHOLIEKE.
Breakefield XO, Brunner HG;
WPI; 98-427102/36.
                                                      Genetic display.

mono:amine oxidase enzyme
Disclosure; Column 47-50; 30pp; English.

A genetic defect linked to pll-p2l of the X chromosome, especially
mutation C936T in exon 8 of the monamine oxidase (MAD) gene is relate
abnormal behaviour. MAD metabolises serotonin, dopamine and
noradrenaline, neurotransmitters whose metabolism is known to affect
behaviour. Disregulation of these transmitters leads to borderline
behaviour. Disregulation of these transmitters are discluding impulsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9520872-A1.
10-AUG-1995.
02-FEB-1995; U01477.
04-FEB-1994; US-192272.
04-FEB-1994; US-191494.
05-AUG-1994; US-286872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the growth of the transgenic abalone. Transgenic molluscs created in this manner can be used to carry DNA whose product promotes growth enhancement, e.g. a gene encoding a growth factor esp. an insulin-like growth factor. Sequences whose product affects the taste or texture of mollusc tissue can also be introduced in this way. Polyploid organisms can be created by treating the fertilised egg with cytochalasin B. If its citilised egg is diploid the resulting polyploids are triploid or tetraploid. These polyploid organisms have enhanced growth properties relative to the same organism with a normal chromosome complement. Triploids allow for the production of sterile seed stock, thereby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overcoming environmental concerns. Sequence 210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New transgenic molluscs, esp. abalone - contg. a DNA sequence heterologous to the mollusc, esp. for enhancing growth properties Example 1; Page 38-39; 61pp; English.

This sequence represents the cohe salmon growth hormone (csGH). The DNA encoding this sequence was included in a vector used to create transgenic molluscs (especially abalone). In the vector pLH2 the encoding sequence is under the control of the actin promoter ACT5-C. This vector increased in the control of the actin promoter ACT5-C. The sector increased in the control of the actin promoter ACT5-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               noradrenaline; mental retardation; impulsive aggression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monamine oxidase A; abnormal behaviour; serotonin; dopamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W61278 standard; Protein; 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; Q98905.
                                                                                                                                                                                                                                                                                                                                                          Genetic diagnosis of impulsive aggression - uses mutant forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 95-283542/37.
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Sequence
   genetic diagnosis of abnormal behaviour.
Sequence 527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V27798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MADS/) MADSEN A L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 DSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVED 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hereford L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 98;
Pred. No.
20; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15; Length 210; 5.60e+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                           is related to
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Query Match
Best Local Similarity

3.0%; 19.3%;

Score 99; Pred. No.

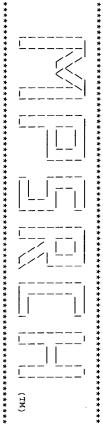
; DB 33; . 4.85e+01;

Length 527

밁 δÃ В δÃ B Ş Matches 369 GAYVAQYYITWNELSYDHQGKEVLTPKAWD 398 310 VEDLIQEGSRFTADHPGLPISYTTSFLRDNV-VATFQNSTDYVETKVTAYRNGDLLLDHS 250 LETISKSDEVEAAFEALIKGVKVAPQTEWKQILDNIEVKAVILGGDPSSGARVVTGKVDM 309 119 iayl-dynnlwrti--dnmgkeiptdapwe 145 60 v-dyvdvggayvgptqnrilrlskelgietykvnvserlvqyvkgktypfrgafppvwnp 118 1 menqekasiaghmfdvvvigggisglsaak-llteygvsvlvleardrvggrtytirneh 59 29; Conservative 40; Mismatches 75; Indels 6. Gaps

Search completed: Mon Aug 30 16:09:55 1999 Job time: 92 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 30 16:07:06 1999; MasPar time 20.87 Seconds 904.473 Million cell updates/sec

Tabular output not generated.

Description:
Perfect Score:
Sequence: >US-09-120-044-3
(1-471) from US09120044.pep
3299.
1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 50.559; Variance 111.373; scale 0.454

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Infect. Immun. (1988) 56:3228-3234

#journal Infect. Immun. (1988) serichia coli of the title Cloning and expression in Escherichia coli of the perfringolysin O (theta-toxin) gene from Clostridium perfringens and characterization of the gene product.

#cross-references MUID:89032622
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FERENCE A43577
#authors Shimizu, T., Okabe, A.; Minami, J.; Hayashi, H.
#journal Infect, Immun. (1991) 59:137-142
#title An upstream regulatory sequence stimulates expression of the perfringolysin O gene of Clostridium perfringens.
#cross-references_MUID:91099951
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Infect. Immun. (1988) 56:3235-3240
Nucleotide sequence of the gene for perfringolysin O
(theta-toxin) from Clostridium perfringens: significant homology with the genes for streptolysin O and pneumolysin.
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perfringolysin O precursor - Clostridium perfringens
#formal_name Clostridium perfringens
03-Feb-1993 #sequence_revision 03-Mar-1993 #text_change
  #length
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                                        #domain signal sequence #status predicted #label SIGV #product perfringolysin O #status experimental #label
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Best Local Similarity 46.9%;
                                                                                                                                                              #authors Domann, E.; Chakraborty, T.
#journal Nucleic Acids Res. (1989) 17:6406
#title Nucleotide sequence of the listeriolysin gene
#monocytogenes serotype 1/2a strain.
#cross-references_MUID:89366684
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#accession A43505
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                                   ##experimental_source strain EGD
##note this sequence is
                                                                             ##cross-references EMBL:X15127;
                                                                                                                                                                                                                                                                                                               ##cross-references GB:M24199; NID:g149652; PID:g149653
##note this sequence is derived from a strong
                                                                                                     ##residues
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A47606
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Infect. Immun. (1988) 56:766-77
Expression in Escherichia coli
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listeriolysin O precursor - Listeria monocytogenes
#formal_name Listeria monocytogenes
21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change
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Geoffroy, C.; Gicquel-Sanzey, B.; Baquero, F.; Perez-Diaz,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              pression in Escherichia coli and sequence analysis of the listeriolysin O determinant of Listeria monocytogenes.
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                                                                                                     1-529 ##label DOM
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               serotype 1/2a
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#accession S12400
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                                                                                                                                             AKECTGLAWEWWRTVIDDRNLPLVKNRNISIWGTTLYPKYSNKVDN 526
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                                                                                                                                                                                                                                                                                          GNLGDLRDILKKGATFNRETPGVPIAYTTNFLKDNELAVIKNNSEYIETTSKAYTDGKIN 420
                                                                                                                                                                                                                                                                                                                                                      QVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                      IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN
                                                                                                                                                                                      LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
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Attenuated mutants of the intracellular bacterium Listeria monocytogenes obtained by single amino acid substitutions in listeriolysin O.
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Identification of the structural gene encoding the SH-activated hemolysin of Listeria monocytogenes:
listeriolysin O is homologous to streptolysin O and
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Cossart, P.
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#product listeriolysin 0 #status predicted #label 
#length 529 #molecular-weight 58688 #checksum 719
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S24231 #ty
listeriolysin
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    #type complete
  precursor
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  Listeria monocytogenes (strain
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#accession S24231
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##experimental_source strain 12067, serotype 4b
##anote sequence was submitted to
Library, June 1991
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Similarity 43.1%; Pred. No. 7.01e-260;
201; Conservative 120; Mismatches 144;
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Listeria monocytogenes isolates can be classified into two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #formal_name Listeria monocytogenes
strain 12067
22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
13-Sep-1998
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$22341 #type complete ivanolysin precursor · Listeria ivanovii #formal_name Listeria ivanovii 07-apr-1994 #sequence_revision 07-apr-19
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07-Apr-1994 #text_change
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#journal Biochim. Biophys. Acta (1992) 1130:81-84
#title Listeriolysin genes: complete sequence of 110 from Listeria
#title ivanovii and of 1so from Listeria seeligeri.
#TOTES-references MUID:92182018
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##residues 1-319,'T',321-528
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##residues 1-528 ##label HAS
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                                                                                                                                                                                                                                                                       LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIFVKLSTSSHSTRVKAAFDAAFKGKSVKGDTELENIIQNASFKAVIYGGSAKDEVEIID 359
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Similarity 43.3%;
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                                          $22340 #type complete
seeligeriolysin - Listeria seeligeri
#formal_name Listeria seeligeri
22.Nov-1993 #sequence_revision 01-Dec-1995 #text_change
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#length 528  #molecular-weight 58511  #checksum 6874
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Best Local Similarity 43.1%;
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##residues 1-501 ##label GEO
##cross-references GB:M62709; NID:g142472; PID:g142473
#length 501 #molecular-weight 55268 #chec
                                                                 ##molecule_type DNA
                                                                                             ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 QVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT 304
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                                                                                                                                                                      Geoffroy, C.; Mengaud, J.; Alouf, J.E.; Cossart, P. J. Bacteriol. (1990) 172:7301-7305
Alveolysin, the thiol-activated toxin of Bacillus alvei, homologous to listeriolysin O, perfringolysin O, pneumolysin, and streptolysin O and contains a single
                                                                                                                 A37858
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alveolysin - Bacillus alvei
#formal_name Bacillus alvei
28-Jun-1991 #sequence_revision
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Biochim. Biophys. Acta (1992) 1130:81-84
Listeriolysin genes: complete sequence of ilo from Listeria
ivanovii and of lso from Listeria seeligeri.
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Pred. No. 1.59e-250;
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  #checksum 8775
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                                                                                                                                                                                                                                                                                                                                                               #cross-references MUID:88057628
                                                                                                                                                                                                                                                       ##residues 1-571 ##label KEH
##cross-references GB:M18638; NID:g153810; PID:g153811
# #length 571 #molecular-weight 63638 #checksum
                                                                                                                                                                                                                                                                                                    *#molecule_type DNA
##residue
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                                                                                                                                                                                                        Match 43.5%;
Local Similarity 42.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAYVAQFEVYWDEFSYDADGQEIVTRKSWDGNWRDRSAHFSTEIPLPPNAKNIRIFAREC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IAGLNYNRNEVLAIQGDQISS-FVPKEGIQSNGKFIVVERDKKSLTTSPVDISIVDSITN 102
              TAIDNLVNQWHDNYSGGNTLPARTQYTESMYYSKSQIEAALNVNSKILDGTLGIDFKSIS 286
                                                                                  SVTDRTYPAALQLANKGFTENKPDAVVTKRNPQKIHIDLPGMGDKAT-VEVNDPTYANVS 226
                                                                                                                     VNDFILAMNYDKKKLLTHQGESIENRFI-KEGNQLPDEFVVIERKKRSLSTNTSDISVTA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILAMNYDKKKLLTHQGESIENRFI-KEGNQLPDEFVVIERKKRSLSTNTSDISVTATNDS
                                                TNDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 45.2%;
l Similarity 42.3%;
192; Conservative
                                                                                                                                                                                           195;
                                                                                                                                                                                                                                                                                                                                                                                            Kehoe, M.A.; Miller, L.; Walker, J.A.; Boulnois, G.J. Infect. Immun. (1987) 55:3228-3232

Nucleotide sequence of the streptolysin O (SLO) gene: structural homologies between SLO and other
                                                                                                                                                                                                                                                                                                                                                   A43507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     streptolysin Oprecursor - Streptococcus pyogenes
#formal_name Streptococcus pyogenes
28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change
09_Sep-1997
                                                                                                                                                                                       Conservative 108; Mismatches 152; Indels
                                                                                                                                                                                                                                                                                                                                                                               membrane-damaging,
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Pred. No. 1.28e-248;
127; Mismatches 132;
                                                                                                                                                                                                        Score 1436; DB 2; 1
Pred. No. 6.09e-238;
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                                                                                                                                                                                                                        Length 571;
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#title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #cross-references MUID:94341910
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      304
                            342 TKDENEIRNIIKDNAELSFKNPAYPISYTSTELKDNATAAVHNNTDYIETTTTEYSSAKM 401
                                                                                                                                                                                                                                                      124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues 1-485 ##label RES
##cross-references GB:D21270; NID:g418066; PID:g600252
# #length 485 #checksum 3782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **status preliminary; translated from GB/EMBL/DDBJ
##molecule_type DNA
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TGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDL
                                                                                                            RTVYVKLETTSKSKDVQAAFKALLKNNSVETSGQYKDIFEESTFTAVVLGGDAKEHNKVV 341
                                                                                                                                                                  HSGEKQIQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYG
                                                                                                                                                                                                           ANGEKKVMVAAYKQIFYTVSAELPNNPSDLFDNSVTFGELTRKGVSNSAPPVMVSNVAYG
                                                                                                                                                                                                                                                 RGAVNDLLAKWHQDYGQVNNVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSV 183
                                                                                                                                                                                                                                                                           AGAVDDLVSTWNEKYSATHTLPARMQYTESMVYSKAQIASALNVNAKYLDNSLNIDFNAV 221
                                                                                                                                                                                                                                                                                                                                    ATNDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSV 123
                                                                                                                                                                                                                                                                                                                                                                          DSVANRTYPGAVQLANKAFADNQPSLLVAKRKPLNISIDLPGMRKENT-ITVQNPTYGNV 161
                                                                                                                                                                                                                                                                                                                                                                                                                    AVNDFILAMNYDKKKLLTHQGESIENRFI-KEGNQLPDEFVVIERKKRSLSTNTSDISVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIDTGIGNLTYNNQEVLAVNGDKVES-FVPKESINSNGKFVVVDVRKNHLQRHQSIFRLL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVFVKLETSSKSNDVEAAFSAALKGTDVKTNGKYSDILENSSFTAVVLGGDAAEHNKVVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAVNDLLAKWHQDYGQVNNVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
                                                                                  RQVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2h 41.2%; Score 1358; DB 2; I
Similarity 40.1%; Pred. No. 4.28e-223;
175; Conservative 121; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yutsudo, T.; Okumura, K.; Iwasaki, M.; Hara, A.; Kakitani, S.; Minamide, W.; Igarashi, H.; Hinuma, Y.
Infect. Immun. (1994) 62:4000-4004
The gene encoding a new mitogenic factor in a Streptococcus pyogenes strain is a distributed only in group A streptococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139863 #type fragment
hemolysin - Bacillus cereus (fragment)
#formal_name Bacillus cereus
19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-Jul-1996
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##molecule_type DNA
##molecules 1-112 ##label SEG
##cross-references EMBL:236908; NID:g535307; PID:g535308
##cross-references EMBL:336908; NID:g535307; PID:g535308
##cross-references EMBL:36908; NID:g535307; PID:g535308
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                                                                                                                                                                                                                                                                                          ##residues 1-96 ##label SEG
##cross-references EMBL:Z36907; NID:g535305; PID:g535306
## #length 96 #molecular-weight 10471 #checksur
                                                                                                                                                                                                                                                                                                                              ##molecule_type DNA ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 ATNDSRLYPGALLVVDETLLENNPTLLAV 92
                                                                                                                                    61
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Local Similarity 50.9%;
les 57; Conservative
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                                                                                                                                                               KAVNDFILAMNYDKKKLLTHQGESIENRFIKEGNQLPDEFVVIERKKRSLSTNTSDISVT 63
$03974 #type complete amine oxidase (flavin-containing) (EC 1.4.3.4) A - bovine monoamine oxidase type A
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#formal_name Streptococcus suis
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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suilysin - Streptococcus suis
#formal_name Streptococcus suis
06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
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Pred. No. 8.99e-
25; Mismatches
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8.99e-17;
tches 33;
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Db 237 NTLNVEFGQANADEGDPTSRTPTLTNIQNINIEVTGTVNTLDL-RDSNDVEKINIHRITK 295
Qy 115 VEDPSNSSVRGAVNDLLAKWHQDYGQVNNVPARMQYEKITAHSME-QLKVKFGSDFEKTG 173
WHSNPEHPGKAYELTTNTDNATANVFNAPMK-HNPGGTDRIMTLQSSDKLTGDYS
Query Match 3.6%; Score 118; DB 3; Length 1361; Best Local Similarity 22.0%; Pred. No. 1.03e-01; Matches 41; Conservative 49; Mismatches 86; Indels 10; Gaps 10;
SUMMARY #length 1361 #molecular-weight 144385 #checksum 6731
##status pre ##residues 1-1 ##cross-references
A new member of the S-layer prote of the crs gene from Campylobac T03415
ERENCE #authors
o-Mar-1999
Shayer protein - Campylobacter rectus S-layer protein - Campylobacter rectus #formal_name Campylobacter rectus
03415
Qy 369 GAYVAQYYITWNELSYDHQGKEVLTPKAWD 398
-DYNNLWRTM DNMG
Qy 310 VEDLIQEGSRETADHPGLPISYITSF-LRDNVVATFQNSTDYVETKVTAYRNGDLLLDHS 368
Db 60 V-DYVDVGGAYVGDTQNRILRLSKQLGLETYKVNVNERLVHYVKGKTYPERGAFPPVWNP 118
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Db 1 MESLQKTSDAGQMFDVVVIGGGISGLSAAK-LLAEHEVNVLVLEARERVGGRTYTVRNEH 59
Query Match 3.8%; Score 124; DB 2; Length 527; Best Local Similarity 20.0%; Pred. No. 1.95e-02; Matches 30; Conservative 42; Mismatches 72; Indels 6; Gaps 5;
SUMMARY #length 527 #molecular-weight 59800 #checksum 6598
##
S FAD; flavoprotein; mitochondrion; oxidoreductase
##molecule_type mxwA ##residues 1-527 ##label POW ##ross-references GB:X15609; NID:q523; PID:q524
##status not
oxidase type B and other flavoenzymes.
#title The primary structure of bovine monoamine oxidase type A. Comparison with perfide sequences of bovine monoamine
Powell, J.F.; Hsu, Y.P.P.; Andrikopoulos, K.; Mallet
RENCE

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                                                                                                                                                                                                                                 143 SLNKGGSSLSPDKSSLESPTMLKLSTDSKPFSYQEPLPKLSRSSS 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##cross-references EMBL:X92441; NID:g1050762; PID:g1050772
##note the nucleotide sequence was submitted to the EMBL Data
Library, October 1995
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NCE S71713
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                                                                                                                                                                                                                                                                                                                     85 PMKLFVTESLLNNQ-HPR-SRSTDDAVSLQDNNLALLEDHRNKPLLSINTDPGVTGVDSS 142
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Local Similarity 27.6%;
es 29; Conservative
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  nucleolar protein NOP5 - yeast (Saccharomyces cerevisiae)
protein 06108; protein YOR310c
#formal_name Saccharomyces cerevisiae
13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boyer, J.; Fairhead, C.; Gaillon, L.; Galisson, F.; Michaux, G.; Thierry, A.; Dujon, B. submitted to the Protein Sequence Database, July 1996 S67113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galisson, F.; Dujon, B. submitted to the EMBL Data Library, October 1995 sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of the yeast Saccharomyces cerevisiae.
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hypothetical protein YOR220w - yeast (Saccharomyces
cerevisiae)
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24-Sep-1998
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                                                                                                  #type complete
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Pred. No. 1.35e-01;
28; Mismatches 41; Indels
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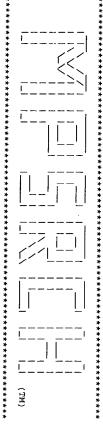
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                                  300 ARVVTGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYR 359
                                                                       245 TEITOTDIDNINALAEQIVEFAAYREQLS-NYLSARMKAIAPNLTQLVGELVGARLIA-H 302
                                                                                                                                                                   188 YGWH-FPELAKIV-TDSVAYARIILTMGIRSKASETDLSEILPEEIEER-VKTAAEVSMG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1511 ##label PEF ##cross-references EMBL:X90565; NID:g940836; PID:g940841 the nucleotide sequence was submitted to Library, August 1995
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##residues 1-511 ##label PEW
##cross-references EMBL:275217; NID:g1420680; PID:e252143; PID:g1420682;
##cross-references EMBL:275210c
303 SGSLISLAKSPASTIQ 318
                                                                                                                       242 YGRQVYLKLETTSKSDEVEAAFEALIKGVKV-APQTEWKQIL-DNTEVKAVILGGDPSSG 299
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##residues 1-511 ##label PEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalogeropoulos, A.; Schweizer, M.
Yeast (1996) 12:1021-1031
Sequencing of a 35.71 kb DNA segment on the right arm of yeast chromosome XV reveals regions of similarity to chromosomes I and XIII.
                                                                                                                                                                                                                                                                                                    #length 511 #molecular-weight 56956 #checksum 4899
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Aug 30 16:04:38 1999; MasPar time 14.67 Seconds 907.352 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: >US-09-120-044-3 (1-471) from US09120044.pep 3299

1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11 Sequence:

77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 51.760; Variance 98.133; scale 0.527

SUMMARIES

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CLATHRIN HEAVY CHAIN. GENOME POLYPROTEIN [CO	DNA-DIRECTED RNA POLYM	TRANSCRIPTIONAL REGULA	HYPOTHETICAL 78.8 KD P	ARACHIDONATE 12-LIPOXY	EUKARYOTIC TRANSLATION	HYPOTHETICAL PROTEIN M		GTP CYCLOHYDROLASE II	GLYCINE CLEAVAGE SYSTE	BETA-GALACTOSIDASE (EC	1A PROTEIN [CONTAINS:	AMINOPEPTIDASE N (EC 3	옄	AMINE OXIDASE [FLAVIN-	NAM8 PROTEIN.		FLAGELLIN (PHASE-1-D F	ARGINASE (EC 3.5.3.1).	REPEAT ELEMENT PROTEIN	
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ALIGNMENTS

TACY_STRPN STANDARD; PRT; 470 AA. P11990; 01-OCT-1989 (REL. 12, CREATED) 01-OCT-1989 (REL. 12, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 15-JUL-1998 (REL. 12, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL-1998 (REL-1988) 15-JUL-1998 (REL-1998) 15-JUL-19	RESULT	III 1				
	ij	TACY_STRPN	STANDARD;	PRT;		
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	20	STREPTOCOCCU	S PNEUMONIAE.			
	8	BACTERIA; FI	RMICUTES; BACILLU	S/CLOSTI	RIDIUM GROUP; S	TREPTOCOCCACEAE;
	8	STREPTOCOCCU				,
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	RP		N.A.			
	RC	STRAIN-NTCC	7466 SEROTYPE II;			
	RX	MEDLINE; 8719	93109.			
	RA	WALKER J.A.,	ALLEN R.L., FALM	MAGNE P.,		BOULNOIS G.J.;
	RT	"Molecular c	loning, character	ization,	and	nucleotide
	RΤ	sequence of t	the gene for pneu	molysin,		
	RT	of Streptoco	cus pneumoniae."	••		
	Ä	INFECT. IMMUR	V. 55:1184-1189(1	987).		
	င္ပ	-!- FUNCTION	SULFHYDRYL-ACTI	VATED TO	XIN. IS ABLE TO	O LYSE CHOLESTEROL
	S	CONTAINI	NG MEMBRANES. CAN	I BE REVI	RSIBLY INACTIV	ATED BY OXIDATION.
	6	CHOLESTE	OL IS THE RECEPT	OR FOR 1	HE BINDING OF	THESE TOXINS TO
	S	EUKARYOT	IC CELL MEMBRANES	•		
	G	-!- SIMILARI	Y: BELONGS TO TH	E THIOL-	ACTIVATED CYTO:	LYSIN FAMILY.
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	င္ပ	the European	Bioinformatics I	institute	. There are n	o restrictions on i
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	38	entities requ	ires a license a	greement	(See http://w	ww.isb-sib.ch/announc

SQ FT INIT_MET ACT_SITE SEQUENCE EMBL; X52474; G47404; -.
EMBL; M17711; G153692; -.
PIR; A28568; A28568.
PROSITE; P800481; THIOL_CYTOLYSINS; 1.
PFAM; PF01289; Thiol_Cytolysin; 1.
HSSEP; P1995; 1PFO.
TOXIN; HEMOLYSIS; CYTOLYSIS. or send an email to license@isb-sib.ch). 427 427 I 470 AA; 52768 MW; BINDING TO CHOLESTEROL (BY SIMILARITY).; D3F3A252 CRC32; its its way bial

Query Match 99.6%; Score 3286; DB 1; Best Local Similarity 99.8%; Pred. No. 0.00e+00; Length 470;

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P1995;
01-FEB-1991
                                                                   OHNO-IWASHITA Y., IWAMOTO M., MI "Cold-labile hemolysin produced from Clostridium perfringens.";
                                                                                                                                                                                                                                               "Nucleotide sequence of the gene for perfringolysin O from Clostridium perfringens: significant homology wit streptolysin O and pneumolysin"; INFECT. IMMUN. 56:3235-3240(1988).
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
STRAIN=ATCC 13124;
MEDLINE; 89032623.
                                                 BIOCHEMISTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHIMIZU T., OKABE A., MINAMI J., HAYASHI H.;
"An upstream regulatory sequence stimulates expression
perfringolysin O gene of Clostridium perfringens.";
INFECT. IMMUN. 59:137-142(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 91099951.
SEQUENCE
                                                                                                                                                                                                     SEQUENCE OF 29-45
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SHIMIZU T., KOBAYASHI T., BA-THEIN W., OHTANI K., HAYASHI H.;

"Sequence analysis of flanking regions of the pfoA gene of

Clostridium perfringens: beta-galactosidase gene (pbg) is located
the 3'-flanking region.";

MICROBIOL. IMMUNOL. 39:677-686(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROY entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                             SEQUENCE
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EMBL; M36704; G144884; -.
EMBL; D49537; G1502275; -.
PIR; B43577; B43577.
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ROSSJOHN J., FEIL
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MEDLINE; 96123363
                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                      PDB; 1PFO; 05-AUG-98.
PROSITE; PS00481; THIOL_CYTOLYSINS; PFAM; PF01289; Thiol_cytolysin; 1.
TOXIN; HEMOLYSIS; CYTOLYSIS; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             model
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"Crystallization and pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of a cholesterol-binding, thiol-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IWAMOTO M., OHNO-IWASHITA Y., ANDO S.; Role of the essential thiol group in from Clostridium perfringens.", EUR. J. BIOCHEM. 167:425-430(1987).
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SUBUNIT: FORMS OLIGOMERS IN THE HOST MEMBRANE
              KVSGAIDELVSKWNEKYSSTHTLPARTQYSESMVYSKSQISSALNVNAKVLENSLGVDFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l of its membrane form.";
89:685-692(1997).
                                         VTATNDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNS
                                                                                                                          NOSIDSGISSLSYNRNEVLASNGDKIES-FVPKEGKKAGNKFIVVERQKRSLTTSPVDIS
                                                                     IIDSVNDRTYPGALQLADKAFVENRPTILMVKRKPININIDLPGLKGENS-IKVDDPTYG
                                                                                                NKAVNDFILAMNYDKKKLLTHQGESIENRFI-KEGNQLPDEFVVIERKKRSLSTNTSDIS
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                                                                                                                                                      110; Mismatches 132;
                                                                                                                                                                 Score 1618; DB 1; Pred. No. 0.00e+00;
                                                                                                                                                                                                                        BINDING TO CHOLESTEROL.
D -> K (IN REF. 3).
K -> I (IN REF. 3).
RKP -> EA (IN REF. 2).
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                                                                                                                                                                                                                                                                                                          3D-STRUCTURE
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s of a thiol-activated
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-!- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.

-!- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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P13128; Q48747; Q57096; Q57206;

O1-JAN-1990 (REL. 13, CREATED)
O1-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
LISTERIOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
HLY OR LISA OR HLYA.
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STRAIN=F2365, F5782 (SEROTYPE 4B), AND F4233, F6789 (SEROTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RASMUSSEN O.F., BECK T., OLSEN J.E., DONS L., ROSSEN L.; "Listeria monocytogenes isolates can be classified into two types according to the sequence of the listeriolysin gene."; INFECT. IMMUN. 59:3945-3951(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence of the listeriolysin monocytogenes serotype 1/2a strain."; NUCLEIC ACIDS RES. 17:6406-6406(1989).
                                                                                                                                                                                                                                                                                                                                                             VINES A., SWAMINATHAN B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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LISTERIA MONOCYTOGENES.
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             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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89366684.
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         institutions as long
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There are no rest
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SIGNAL
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;; M24199; G149653; -.
;; X60035; G44112; -.
;; U25452; G887807; -.
;; U25443; G887016; -.
;; U25446; G887804; ALT_INIT.
;; U25449; G887864; ALT_INIT.
                                                                                                                                             AKECTGLAWEWWRTVIDDRNLPLVKNRNISIWGTTLYPKYSNKVDN 526
                                                                                                                  IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN 470
                                                                                                                                                                                      IDHSGGYVAQFNISWDEVNYDPEGNEIVQHKNWSENNKSKLAHFTSSIYLPGNARNINVY 480
                                                                                                                                                                                                                                                                               QVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
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A43505; A43505
                                                                                                                                                                     LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
                                                                                                                                                                                                                           GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                                                                                                                                                     GNLGDLRDILKKGATFNRETPGVPIAYTTNFLKDNELAVIKNNSEYIETTSKAYTDGKIN
                                                                                                                                                                                                                                                                                                                                                               EGKMQEEVISFKQIYYNVNVNEPTRPSRFFGKAVTKEQLQALGVNAENPPAYISSVAYGR
                                                                                                                                                                                                                                                                                                                                                                                          AVNDLLAKWHQDYGQVN-NVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                               NDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n 47.2%;
Similarity 43.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   529 AA;
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438
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V -> I (IN STRAINS F2365, F F6789 AND 12067).
K -> S (IN STRAINS F2365, F F6789 AND 12067).
W; 269EA737 CRC32;
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Pred. No. 4
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S -> L (IN STRAINS F2365,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; DB 1;
4.39e-303;
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031831;
01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
IVANOLYSIN PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).

STANDARD;

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Best Local S
Matches 20
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SEQUENCE
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MEDLINE; 92182018.
HAAS A., DUMBSKY M., KREFT J.;
"Listeriolysin genes: complete sequence of ilo from Listeria ivanovii "Listeriolysin genes: complete sequence of ilo from Listeria seeligeri.";
and of lso from Listeria seeligeri.";
BIOCHIM. BIOPHYS. ACTA 13078171807 MOYTN TO DIFF TO LYCE CHOLESTEROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00481; THIOL_CYTOLYSINS; 1. PFAM; PF01289; Thiol_cytolysin; 1. HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BACTERIA; FIRMICUT
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SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDQYIQGLDYDKNNILVYDGEAVKNVPPKAGYKEGNQYIVVEKKKKSINQNNADIQVINS 119
  IRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKVEN 470
                                                                                                   LDHSGAYVARFNVTWDEVSYDANGNEVVEHKKWSENDKDKLAHFTTSIYLPGNARNINIH 479
                                                                                                                                                          GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                                                                                                                                                                          DIFVKLSTSSHSTRVKAAFDTAFKGKSVKGDTELENIIQNASFKAVIYGGSAKDEVEIID 359
                                                                                                                                                                                                                                                                                                                                                                                            AVNDLLAKWHQDYGQVN-NVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH 184
                                                                                                                                                                                                                                                                                                                                                                                                                                GVNTLVDRWNNKYSEEYPNISAKIDYDQEMAYSESQLVAKFGAAFKAVNNSLNVNFGAIS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LASLTYPGALVKANSELVENOPDVLPVKRDSVTLSIDLPGMVNHDNEIVVQNATKSNIND 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNDFILAMNYDKKKLLTHQGESIENRFIKEGNQLPDEFVVIERKKRSLSTNTSDISVTAT 65
                                      AKECTGLAWEWWRTVVDDRNLPLVKNRNVCIWGTTLYPAYSDTVDN 525
                                                                               LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
                                                                                                                                                                                             GDLSKLRDILKQGANFDKKNPGVPIAYTTNFLKDNQLAVVKNNSEYIETTSKAYSDGKIN 419
                                                                                                                                                                                                                                     QVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                                                                                                                                                                                                   SGEKQIQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYGR
                                                                                                                                                                                                                                                                                                                                                     EGKVQEEVINFKQIYYTVNVNEPTSPSRFFGKSVTKENLQALGVNAENPPAYISSVAYGR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 46.7%;
Similarity 43.1%;
201; Conservative
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483
528 AA;
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528 T
483 B
58542 MW;
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Pred. No. 7.16e-299;
122; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING TO CHOLESTEROL (BY SIMILARITY).; CFAE84AD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVANOLYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 528;
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01-JUL-1993 (REL. 26, CREATED)
01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
SEELIGERIOLYSIN PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOXIN;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X60462; G44145; -.
PIR; S22340; S22340; S22340; THIOL_CYTOLYSINS; 1.
PROSITE; PS00481; THIOL_CYTOLYSIN; 1.
HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Listeriolysin genes: complete sequence of ilo from Listeria ivanovii and of lso from Listeria seeligeri.";
BIOCHIM. BIOPHYS. ACTA 1130:81-84(1992).
-i- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAAS A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISTERIA SEELIGERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                             126
422 IDHSGGYVAQFNISWDEVSYDENGNEIKVHKKWGENYKSKLAHFTSSIYLPGNARNINIY 481
                                305 GKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLL
                                                                                                                                                                                                                                                                              182 AVNTLVERWNDKYSKAYPNINAKIDYSDEMAYSESQLIAKFGTAFKAVNNSLNVNFEAIS
                                                                                                                                                                                                                                                                                                                                                 122 ISSLTYPGALVKANRELVENQPNVLPVKRDSLTLSVDLPGMTKKDNKIFVKNPTKSNVNN 181
                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                    62 INKYIWGLNYDKNSILVYQGEAVTNVPPKKGYKDGSEYIVVEKKKKGINQNNADISVINA 121
                                                                                                                                                                                                                                                                                                                                                                                   6 VNDFILAMNYDKKKLLTHQGESIENRFIKEGNQLPDEFVVIERKKRSLSTNTSDISVTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTIC CELL MEMBRANES. SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                              DGKVQEEVISFKQIYYNINVNEPTSPSKFFGGSVTKEQLDALGVNAENPPAYISSVAYGR 301
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                                                                 GNLGELRDILKKGSTYDRENPGVPISYTTNFLKDNDLAVVKNNSEYIETTSKSYTDGKIN 421
                                                                                                     QVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVT
                                                                                                                                       QVYVKLSSSSHSNKVKTAFEAAMSGKSVKGDVELTNIIKNSSFKAVIYGGSAKEEVEIID
                                                                                                                                                                          SGEKQIQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYGR
                                                                                                                                                                                                                                           AVNDLLAKWHQDYGQVN-NVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVH
                                                                                                                                                                                                                                                                                                                  NDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%;
Similarity 43.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DUMBSKY M., KREFT J.;
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26
485
530 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No. 1.13e-290;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOXIN; HEMOLYSIS; CYTOLYSIS; SIGNAL.

SIGNAL
1
2
POTENTIAL.

CHAIN
3
501
ACT_SITE
461
461
BINDING TO
CONFLICT
56
56
A -> L (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF01289; Thiol_cytolysin; 1. HSSP; P19995; 1PFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STUTTGART (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALOUF J.E., GEOFFROY C., GILLES A.M., FALMAGNE P.;
(IN) RAPPUOLI R., ALOUF J.E., FALMAGNE P. (EDS.);
BACTERIAL PROTEIN TOXINS, PP.49-50, GUSTAV FISHER VERLAG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEOFFROY C., MENGAUD J., ALOUF J.E., COSSART P.;
"Alveolysin, the thiol-activated toxin of Bacillus alvei, is
homologous to listeriolysin O, perfringolysin O, pneumolysin,
streptolysin O and contains a single cysteine.";
J. BACTERIOL. 172:7301-7305(1990).
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01-NOV-1991 (REL. 20, CREATED)
01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M62709; G142473; -.
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                                         162
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                                                                                                                                                                                                                                                        44 IAGLNYNRNEVLAIQGDQISS-FVPKEGIQSNGKFIVVERDKKSLTTSPVDISIVDSITN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.
SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
QLVSTWGEKYSSTHTLPARLQYAESMYYSONQISSALNVNAKVLNGTLGIDFNAVANGEK
                                                                                     RLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNSSVRGAVN
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                                                                                                                                     RTYPGAIQLANKDFADNQPSLVMAARKPLDISIDLPGLKNENT-ISVQNPNYGTVSSAID 161
                                                                                                                                                                                                   ILAMNYDKKKLLTHQGESIENRFI-KEGNQLPDEFVVIERKKRSLSTNTSDISVTATNDS
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                                                                                                                                                                                                                                                                                                                            192;
                                                                                                                                                                                                                                                                                                                      h 45.2%;
Similarity 42.3%;
192; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    501 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THIOL_CYTOLYSINS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    55268 MW;
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                                                                                                                                                                                                                                                                                                                Score 1492; DB 1; I
Pred. No. 1.85e-288;
127; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                    A -> L (IN REF. 2).
; 8DF2C94A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING TO CHOLESTEROL
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                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 95102113.

OKUMURA K., HARA A., TANAKA T., NICHIGUCHI I., MINAMIDE W., IGARASHI H., YUTSUDO T.;

"Cloning and sequencing the streptolysin O genes of group C and group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               054114:
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                        SEQUENCE
                                                                                                                        SIGNAL
                                                                                                                                                           PFAM; PF01289; Thic HSSP; P19995; 1PFO.
                                                                                                                                                                       PROSITE; PS00481; THIOL_CYTOLYSINS PFAM; PF01289; Thiol_cytolysin; 1.
                                                                                                                                                                                                           EMBL; D16824; G498301; -
                                                                                                                                                                                                                                                                                                                                                                          EUKARYOTIC CELL MEMBRANES.
-!- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G streptococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA; FIRE
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                                                                                                                                       TOXIN; HEMOLYSIS; CYTOLYSIS; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREPTOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       462 TGLAWEWWRTVVDEYNVPLASDINVSIWGTTLYP 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 GAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVKIREC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 GAYVAQFEVYWDEFSYDADGQEIVTRKSWDGNWRDRSAHFSTEIPLPPNAKNIRIFAREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 MVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYRNGDLLLDHS
   Watch 43.6%;
Local Similarity 42.4%;
nes 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342 VIQSVIKDNAQFSSKNPAYPISYTSVFLKDNSIAAVHNNTEYIETKTTEYSKGKIKLDHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 KLETTSKSNDVQTAFKLLLNNPSIQASGQYKDIYENSSFTAVVLGGDAQTHNQVVTKDFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 QIQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYGRQVYL
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   110;
                  Score 1437; DB 1;
Pred. No. 2.74e-276;
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MEDLINE; 88057628.
KEHOE M.A., MILLER L., WALKER J.A., BOULNOIS G.J.;
"Nucleotide sequence of the streptolysin O (SLO) gene: structural homologies between SLO and other membrane-damaging, thiol-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACY_STRPY STANDARD; PRT; 571 AA. P21131; 01-FEB-1991 (REL. 17, CREATED) 01-FEB-1991 (REL. 17, LAST SEQUENCE UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE) CYT.
                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFECT. IMMUN. 55:3228-3232(1987).

-i- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL-
-i- FUNCTIONING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION.

CONTAINING MEMBRANES. CAN THE BINDING OF THESE TOXINS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREPTOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                                        PFAM; PF01289; Thiol_cytolysin; HSSP; P19995; 1PFO.
                                                                                                                                                                          PROSITE; PS00481; THIOL_CYTOLYSINS;
                                                                                                                                                                                                                     PIR; A43507; A43507
                                                                                                                                                                                                                                                        EMBL; M18638; G153811; -.
                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLASMID PMK157
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SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
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SEQUENCE
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Q53957;
                                                                                                                                                                   DNA SEQ. 4:325-328(1994).

-!- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES.
-!- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                      OKUMURA K., HARA A., IGARASHI H., YUTSUDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREPTOCOCCUS CANIS
                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREPTOLYSIN O PRECURSOR (THIOL-ACTIVATED CYTOLYSIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 95102113.
                                                                                                                                                                                                                                                                                                                                                                                                                    STREPTOCOCCUS
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                                                                                                                                                                                                                                                                                                     "Cloning and sequencing the streptolysin O genes of group C and group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSVK
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571 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 108; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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63638 MW;
                                                                                                                                                                                                                                                                                                                                          TANAKA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1436; DB 1;
No. 4.56e-276;
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Best Local
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                                                                   SUBMITTED (NOV-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.

-i- FUNCTION: SULFHYDRYL-ACTIVATED TOXIN. IS ABLE TO LYSE CHOLESTEROL CONTAINING MEMBRANES. CAN BE REVERSIBLY INACTIVATED BY OXIDATION. CHOLESTEROL IS THE RECEPTOR FOR THE BINDING OF THESE TOXINS TO EUKARYOTIC CELL MEMBRANES (BY SIMILARITY).

-i- FUNCTION: HEMOLYTIC ACTIVITY AGAINST RED BLOOD CELL.

-i- SIMILARITY: BELONGS TO THE THIOL-ACTIVATED CYTOLYSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                 TACY_BACCE
Q45105;
                                                  This
                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                between
                                                                                                                                                                                                                                                                               BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
                                                                                                                                                                                                                  STRAIN=RIMD 206001;
                                                                                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                DACILLOS CEREUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00481; THIOL_CYTOLYSINS;
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                   European Bioinformatics Institute.
                        SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARECTGLAWEWWRKVIDERDVKLSKEINVNISGSTLSP 567
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                                                                                                                                                                                                                                                                                                                SIN PRECURSOR (FRAGMENT).
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Similarity 42.1%;
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574 AA;
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institutions as long
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Pred. No. 1.57e-272;
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BY SIMILARITY.
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as its content
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                 AOFA_BOVIN STANDARD; PRT; 527 AA.

F21398;

F21398;

O1-MAY-1991 (REL. 18, CREATED)

O1-MAY-1991 (REL. 18, LAST SEQUENCE UPDATE)

15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)

AMINE OXIDASE [FLAVIN-CONTAINING] A (EC 1.4.3.4) (MONOAMINE OXIDASE)
                    MEDLINE; 89246344.

POWELL J.F., HSU Y.P.P., WEYLER W., CHEN S., SANDRIKOPOULOS K., MALLET J., BREAKEFIELD XO.

"The primary structure of bovine monoamine oxwith peptide sequences of bovine monoamine oxwith peptide sequences of bovine monoamine oxwith performs.";
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                                                                                                                                                                                                                                             BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE;
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                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          BOS TAURUS
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                                                                                                                                                                                                                                                                                                                                                              (MAO-A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402 TLDHYGAYVAQFDVSWDGFTFDQNGKEILTHKTWEGSGKDKTAHYSTVIPLPPNSKNIKI 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 LLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGNVRNLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 HSGEKQIQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 AGAVDDLVSTWNEKYSATHTLPARMQYTESMVYSKAQIASALNVNAKYLDNSLNIDFNAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 SIDTGIGNLTYNNQEVLAVNGDKVES-FVPKESINSNGKFVVVDVRKNHLQRHQSIFRLL
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11 Similarity 40.1%;

175; Conservation
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259:407-413(1989).
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larity 40.1%; Pred. No. 7.75e-259;
Conservative 121; Mismatches 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMY
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                                                                                                                                                                                                                                                                                  STRAIN=S288C / FY1679;
PEARSON B.M., HERNANDO Y., WOLF S.S., KALC
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q12499;
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X15609; G524; -.
EMBL; X15609; G525; ALT_INIT.
                                                                                     WU P.,
                                                                                                                            MEDLINE;
                                                                                                                                                                  STRAIN=W303
                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 VEDLIQEGSRFTADHPGLPISYTTSF-LRDNVVATFQNSTDYVETKVTAYRNGDLLLDHS 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 LETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKAVILGGDPSSGARVVTGKVDM 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MESLOKTSDAGOMFDVVVIGGGISGISAAK-LLAEHEVNVLVLEARERVGGRTYTVRNEH 59
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SUBCELLULAR LOCATION: MITOCHONDRIAL OUTER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CATALYZES THE OXIDATIVE DEAMINATION OF BIOGENIC AND XENOBIOTIC AMINES AND HAS IMPORTANT FUNCTIONS IN THE METABOLISM NEUROACTIVE AND VASOACTIVE AMINES IN THE CENTRAL MERVOUS SYSTEM AND PERIPHERAL TISSUES. MAO-A PREFERENTIALLY OXIDIZES BIOGENIC AMINES SUCH AS 5-HYDROXYTRYPTAMINE (5-HT), NOREPINEPHRINE AND TEXTURE OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
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BROCKENBROUGH J.S., METCALFE A.C., CHEN is a small nucleolar ribonucleoprotein S rRNA processing in yeast.";
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                                                                                                                                                                                                         AND CHARACTERIZATION
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Pred. No. 2.64e-03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
; 724E4396 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 AA
                                                                                                                                                                                                                                                                                                                                     KALOGEROPOULOS
                                                                                 CHEN S., ARIS J.P.;
                                                                                                                                                                                                                                                                                          DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72; Indels
                                          component required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 527;
                                                                                                                                                                                                                                                                                          BANKS
                                                                                                                                                                                                                                                                                                                                 Α.,
                                                                                                                                                                                                                                                                                                                                 SCHWEIZER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      P75404;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                          STRAIN=ATCC 29342 MEDLINE; 97105885
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=ATCC 29342 / M129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DP3A_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR PROTEIN; RRNA PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                           HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
                                                                                                                                                                                                                                                                                                                                                                              MYCOPLASMA PNEUMONIAE.
                                                                                                                                                                                                                                                                                                                                                                                                             DNA POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998
                                                                                                                                                                                                                                  pneumoniae."
                                                                                                                                                                                                                                                                 HERRMANN R.
                                                                                                                                                                                                                                                                                                                                                    MYCOPLASMATACEAE; MYCOPLASMA
                                                                                                                                                                                                                                              'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 NGDLL-LDHSGAYVAQ 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 SGSLISLAKSPASTIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 ARVVIGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTAYR 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 YGRQVYLKLETTSKSDEVEAAFEALIKGVKV-APQTEWKQIL-DNTEVKAVILGGDPSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 YGWH-FPELAKIV-TDSVAYARIILTMGIRSKASETDLSEILPEEIEER-VKTAAEVSMG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 TEITQTDLDNINALAEQIVEFAAYREQLS-NYLSARMKAIAPNLTQLVGELVGARLIA-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.4%;
Local Similarity 22.8%;
les 31; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; AF056070; G3170533; -. L0004000; NOP5.
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                                                                                                                                                                                                                                                                                                                                                                  FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                  (REL. 35, CREATED)
(REL. 35, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)

8 (REL. 37, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56956 MW;
                                                                                                                                                                                                                                                                                                                                                                  BACILLUS/CLOSTRIDIUM GROUP; MOLLICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 112; DB 1;
Pred. No. 1.09e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                         There are no restrictions ong as its content is in
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                              for commercial
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Best Local
                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLAP_BACST STANDARD; PRT; 1228 AA. p35825; 01-JUN-1994 (REL. 29, CREATED) 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) 5-LAYER PROTEIN PRECURSOR (SURFACE LAYER PROTEIN).
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                  EMBL; X71092; G312730; -. PIR; S34365; S34365. HSSP; P02766; 1ETB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000045; G1674148; -.
TRANSFERASE; DNA-DIRECTED DNA POLYMERASE; DNA REPLICATION SEQUENCE 872 AA; 99257 MW; C6C0C49B CRC32;
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                              SIGNAL; CELL WALL; S-LAYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             surface-layer protein of Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACILLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACILLUS STEAROTHERMOPHILUS. BACILI FIRMICUTES; BACILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
259 VEAAFEALIKGVKVAPQTEWKQI-LDNTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEG 317
                              256 DEAALTPKVESVS-AINTQNKAVELTAVPVNGT-LKLQLSAAANEDTVNVNTVRIYKVDG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 KDKSLL 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 KTGNSLDIDFNSVHSGEKQ-IQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 ETKRDLVIDYVMQKYGREQCAQIVTF-QKF-KTR-SALRDVGKVFNHIEGAEDLLGK-LP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 FLQVEDPSNSSYRG-AVNDLLAKWHQDYGQVNNVPARMQYEKITAHSMEQLKVKFGSDFE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302 FAHNNDILIGPGRGSAVGSLVA-FLLKITQIDPVANNLIFERFISRHRQGLP-DIDIDIM 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AERPLV 235
                                                                                                                                                           y Match 3.3%;
Local Similarity 24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E 145:115-120(1994).

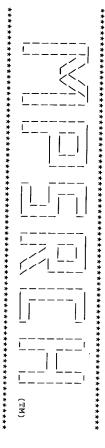
E 145:115-120(1994).

FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS, WHICH COAT THE SURFACE OF BACTERIA.

SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIA IS COVERED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                   YDITV-AMKAR-EV-QDAVKAGNLDKAKAAVDQINQYLPKVTDAFKTELT-EVAKKALDA 255
                                                                  YTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVAYGRQVYLKLETTSKS-DE 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 3.3%;
Similarity 25.4%;
32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94320770
                                                                                                                                                                                                             1228 AA;
                                                                                                                                            Conservative
                                                                                                                                                                                                                               1228
                                                                                                                                                                                                               131076 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LUBITZ W.;
the sbsA gene encoding the 130-kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                   Score 110; DB 1; Length 1228; Pred. No. 1.97e-01; 43; Mismatches 72; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 110; DB 1; Length 872; Pred. No. 1.97e-01; 29; Mismatches 57; Indels
                                                                                                                                                                                                          S-LAYER PROTEIN.
W; ODOFB37F CRC32;
                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                       Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain PV72.";
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                                                                                                                                       Matches
                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        029150;
01-NOV-1997 (REL. 35, CREA
01-NOV-1997 (REL. 35, LAST
01-NOV-1997 (REL. 35, LAST
KAPPA CASEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATESY J., HAYASHI C., CRONIN M., ARCTANDER P.;
SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: KAPPA CASEIN STABILIZES MICELLE FORMATION, PREVENTING
                                                                                                                                                                                                                                         PFAM; PF00997; casein_kappa; 1. MILK; PHOSPHORYLATION; GLYCOPROTEIN.
                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                              EMBL; U53894; G1293141; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CASEIN PRECIPITATION IN MILK.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- TISSUE SPECIFICITY: MAMMARY GLAND; MILK.
-!- SIMILARITY: BELONGS TO THE KAPPA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNCIA UNCIA (SNOW LEOPARD) (PANTHERA UNCIA).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSN3 OR CSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARNIVORA; FISSIPEDIA; FELIDAE; UNCIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CASK_UNCUN
                                136 TTTV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 S-RETADHPGLPISYTTSELRDNVVATEQNSTDY-VETKVTAYRNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 NIPFALNTADVSLSTDGKTITVDASTPFENNTEYKVVVKGIKDKNG
                                                                                                                             3.2%;
Local Similarity 25.0%;
les 16; Conservation
                                                             38 QLPDEFVVIERKKRSLSTNTSDISVTATNDSRLYPGALLVVDETLLENNPTLLAVDRAPM 97
98 TYSI 101
                                                                                              76 HLPASFIVIPPKKIQDKTGNPTINTIATAEPTLTPTTEPIVNTVVTTEASSEFTITSTPE 135
                                                                                                                                                                                                         146 AA; 16337 MW; 8321CFD3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REL. 35, CREATED)
(REL. 35, LAST SEQ
(REL. 35, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE UPDATE)
                                                                                                                                  Score 105; DB 1; Lep
Pred. No. 8.42e-01;
19; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AA
                                                                                                                                                                    Length 146;
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359
                                                                                                                                  0;
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Search completed: Mon Aug 30 16:05:06 1999 Job time: 28 secs.



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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Aug 30 16:05:23 1999; MasPar time 29.10 Seconds 883.456 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-09-120-044-3 (1-471) from US09120044.pep 3299

Sequence: 1 MANKAVNDFILAMNYDKKKL.....TISIWGTTLYPQVEDKVEND 471

Scoring table: PAM 150 Gap 11

179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 49.610; Variance 95.041; scale 0.522

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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PHOSPHATE TRANSPORT AT	L0038.	T16B24.10 PROTEIN.	TRANSPONSON PROTEIN B.	CONSERVED HYPOTHETICAL	CHROMOSOME IV COSMID 9			RIPOTHETICAL 99.2 KD P	00000	CHAINING	95.0 KD	HYPOTHETICAL 49.7 KD P	CHROMOSOME XV READING	S-LAYER PROTEIN.	S-LAYER PROTEIN.	LISTERIOLYSIN O (FRAGM	LISTERICLISIN O (FRAGM		PYOLYSIN	HEMOLYSIN.	SUILYSIN.		Description
2.116+00	2 116+00	6.62e-01	4.93e-01	6.62e-01	1.19e+00	1.19e+00	6.62e-01	2.01e-01	2./IE-01		1.486-01	5.91e-02	2.32e-02	1.69e-02	1.69e-02	1.69e-02	2.46e-03	4.770.401	4 770-251	0.00+00	0.00e+00	1	Pred. No.

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UL37. H05L14.2 PROTEIN.	7-KETO-8-AMINOPELARGON	AT103.	OUTER MEMBRANE PROTEIN	RESTRICTION ENDONUCLEA	COSMID F31D5.	U	X SYSTEM	97.4 KD	HYPOTHETICAL 91.9 KD P	EIN.	HYPOTHETICAL 74.1 KD P	MYOSIN HEAVY CHAIN-LIK	VATED	HYPOTHETICAL 53.3 KD P	CELL DIVISION INHIBITO	HYPOTHETICAL PROTEIN M	GROWTH HORMONE (FRAGME	RORF8.	C04B4.6 PROTEIN.	PROLINE-RICH PROTEIN (C45G7.6 PROTEIN.	PUTATIVE L-AMINO ACID	AMINOTRANSFERASE.
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ALIGNMENTS

209 DAVNSGEKQVQLIVNFKQIYYTYSVDEPESPSKLFAEGTTVEDLKRNGITDEVPPVYVSSV :: : :	
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122 SVRGAVNDLLAKWHODY-GOVNNVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDF	ΩУ
149 TVRTGVNNLLSKWNNTYAGEYGNTQAELQYDETMAYSMSQLKTKFGTSFEKIAVPLDINF	Db
62 VTATNDSRLYPGALLVVDETILENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNS	Qy
89 VIDAKAANIYPGALLRADQNLLDNNPTLISIARGDLTLSLNLPGLANGDSHTVVNSPTRS	Db
	Qy
29 SKQDINQYFQSLTYEPQEILTNEGEYIDNPPATTGMLENGRFVVI.BREKKNTTNNSADTA	망
Query Match 54.8%; Score 1808; DB 2; Length 497; Best Local Similarity 50.4%; Pred. No. 0.00e+00; Matches 236; Conservative 113; Mismatches 117; Indels 2; Gaps	Que Bes Mat
SUBMITTED (OCT-1998) TO EMBL/GENBANK/DDBJ DATA BANKS	
suis, and expression in field strains.":	
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STRAIN=P1/7;	
SEQUENCE OF 1-71 FROM N.A.	
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MBIRET 09 LAST	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                  LSVKIRECTGLAWEWWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKV
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"The Arcanobacterium (Actinomyces) pyogenes hemolysin, novel member of the thiol-activated cytolysin family.", J. BACTERIOL. 179:6100-6106(1997).
EMBL; U84782; G2252800; ".

PFAM: PF01289; Thiol_cytolysin; 1.
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01-JAN-1998 (TREMBLREL.
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ACTINOMYCETALES; ACTINOMYCINEAE; ACTINOMYCETACEAE; ARCANOBACTERIUM:
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BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
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418 VRNLSVKIRECTGLAWE-WWRTVYEKTDLPLVRKRTISIWGTTLYPQVEDKV 468
                                 482 ARNIHVEAGEATGLAWDPWW-TVINKKNLPLVPHREIVLKGTTLNPWVEDNV 532
                                                                         358
                                                                                                         422 YKSGEITFRHGGGYVAKFRLKWDEISYDPQGKEIRTPKTWSGNWAARTLGFRETIQLPAN 481
                                                                                                                                                   298
                                                                                                                                                                                                                        242 YGRQVYLKLETTSKSDEVEAAFEALIKG--VKVAPQ--TEWKQILDNTEVKAVILGGDPS
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                                                                                                                                                                                                                                                                                                                                       242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 AFDANNAHVYPGALVLANKDLAKGSPTSIGIARAPQTVSVDLPGLVDGKNKVVINNPTKS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                62 VTATINDSRLYPGALLVVDETLLENNPTLLAVDRAPMTYSIDLPGLASSDSFLQVEDPSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 40.3%; Local Similarity 40.7%;
                                                                                                                                                                                   GGVEVATGNIDALKKIIKEESTYSTKVPAVPVSYAVNFLKDNQLAAVRSSGDYIETTATT
                                                                                                                                                                                                                                                           YGRQIFVKLETTSTSNDVQAAFSGLFKAKFGNLSTEFKAKYADILNKTRATVYAVGGSAR
                                                                                                                                                                                                                                                                                                SVHSGEKQIQIVNFKQIYYTVSVDAVKNPGDVFQDTVTVEDLKQRGISAERPLVYISSVA
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                                                                         YRNGDLLLDHSGAYVAQYYITWNELSYDHQGKEVLTPKAWDRNGQDLTAHFTTSIPLKGN
                                                                                                                                                                                                                                                                                                                                     AIHKRERQVAIASFKQIYYTASVDTPTSPHSVFGPNVTAQDLKDRGVNNKNPLGYISSVS
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                                                                                                                                                                                                                                                                                                                                                                                                           SVTQGLNGLLDGWIQRNSKYPDHAAKISYDETMVTSKRQLEAKLGLGFEKVSAKLNVDFD 241
                                                                                                                                                   SGARVVIGKVDMVEDLIQEGSRFTADHPGLPISYTTSFLRDNVVATFQNSTDYVETKVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          534 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 125; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thiol_cytolysin; AA; 57873 MW; 1
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Pred. No. 4.77e-251;
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                             Q48772
        STRAIN-11984, TYPE MEDLINE; 96118685
                                                           BACTERIA; FIRMICUTES;
                                                                                          LISTERIOLYSIN O (FRAGMENT).
RASMUSSEN O.F.,
                             SEQUENCE FROM N.A.
                                                 LISTERIA.
                                                                      LISTERIA MONOCYTOGENES
                                                                                                                                              PRELIMINARY;
                   TYPE
 SKOUBOE P.,
                                                             BACILLUS/CLOSTRIDIUM GROUP;
 DONS L.,
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 ROSSEN L.,
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             WANG B., KRAIG E., KOLODRUBETZ D.;
"A new member of the S-layer protein i crs gene from Campylobacter rectus.";
INFECT. IMMUN. 66:1321-1526(1998).
                                                                                                                                                                                                                                                                                                      O30524;

O1-JAN-1998 (TREMBLREL: 05,

O1-JAN-1998 (TREMBLREL: 05,

O1-NOV-1998 (TREMBLREL: 08,
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SEQUENCE
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                                                                                                                                                                                                                                                                   S-LAYER PROTEIN.
CRS.
                                                                                                         MEDLINE; 98187925.
                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                     CAMPYLOBACTER
                                                                                                                                                                                                                                                                                                                                                                                                       030524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Listeria monocytogenes exists in at least three evolutionary evidence from flagellin, invasive associated protein and listeriolysin O genes.";
MICROBIOLOGY 141:2053-2061(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=206.1.1, TY
MEDLINE; 96118685.
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01-NOV-1996 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACTERIA;
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MICROBIOLOGY 141:2053-2061(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RASMUSSEN O.F., SKOUBOE P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 NTEVKAVILGGDPSSGARVVTGKVDMVEDLIQEGSRFTADHPGLPISYT 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISTERIA MONOCYTOGENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NSSFKAVIYGGFAKDEVQIIDGNLGDLRDILKKGATFNRETPGVPIAYT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 3.8%;
Local Similarity 34.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NSSFKAVIYGGSAKDQVQIIDGNLGDLRDILKKGATFNRETPGVPIAYT 50
    AF010143;
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Similarity 34.7%;
17; Conservative
                                                                                                                                                                                                                     PROTEOBACTERIA;
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G2459961;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 118; DB 2;
Pred. No. 1.69e-02;
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Pred. No. 2.46e-03;
14; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A4B59721 CRC32;
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                                                       family: characterization
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| SULT | 8 | Q12044 | PRELIMINARY; | Q12044 | Q12044; | Q12044; | Q12044; | Q1-NOV-1996 (TREMBLREL 01, I 01-NOV-1996 (TREMBLREL 01, I 01-NOV-1996 (TREMBLREL 01, I
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087083;
                                                                                                                                                                                                                                                                                                                                                                                                                       "The S-layer protein from Campylobacter rectus: sequence determination and function of the recombinant protein."; FEMS MICROBIOL LETT. 166:275-281(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIYAMOTO M., MAEDA H., KITANAKA M., KOKEGUCHI S., TAKASHIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-ATCC 33238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA;
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CAMPYLOBACTER RECTUS
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                                                                                                                                                                                                                                                                                                                 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAMPYLOBACTER
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                                                                                                                   290 VILGGD
                                                                                                                                            353 LSITSD 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 LSITSD 358
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Local Similarity 22.0%;
les 41; Conservative
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Local Similarity 22.0%;
                                                                                                                                                                 ERPLVY-ISSVAYGRQVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQILDNTEVKA
                                                                                                                                                                                                                                                 NTLNVEFGQANADEGDPTSRTPTLTNIQNINIEVTGTVNTLDL-RDSNDVEKINIHRITK 295
                                                                                                                                                                                                                                                                               VEDPSNSSVRGAVNDLLAKWHQDYGQVNNVPARMQYEKITAHSME-QLKVKFGSDFEKTG
                                                                                                                                                                                                                                                                                                         VDWHSNPEHPGKAYELTTNTDNATANVFNAPMK-HNPGGTDRIMTLQSSDKLTGDYSRHD 236
                                                                                                                                                                                            EAGNKFNVESIG-QKLVGMRLANVAKKD-IDVKFEH-KKGVLSGFEDKSNVFLENVEAKS
                                                                                                                                                                                                                      NSLDIDENSVHSGE-KQI-QIVNEKQI-YYTVSVDAVKNPGDVFQDTVTVEDLKQRGISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEDPSNSSVRGAVNDLLAKWHQDYGQVNNVPARMQYEKITAHSME-QLKVKFGSDFEKTG
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                                                                                                                                                                                                                                                                                                                                                                                                 1361 AA;
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                                                                                                                                                                                                                                                                                                                                        Pred. No. 49; Misma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 118; DB 2; Le
Pred. No. 1.69e-02;
Pred. wiematches 86;
                                                                                                                                                                                                                                                                                                                                                    Score 118; DB 2; Length 1361; Pred. No. 1.69e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                              55A9D736 CRC32;
                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                       86;
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                                                                                                                                                                                                                                                                                                                                       Indels
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CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)

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291 ILGGDPSSGARVVTGKVDMVEDLIQEGSRFTADHPG--LPISYTTSFLRDNV 340

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                                                                                                                                                                                                                    Query Match
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SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        068518;
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SUBMITTED (OCT-1995) TO
EMBL; Z75128; E252085;
EMBL; X92441; G1050772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BOYER J., FAIRHEAD C., THIERRY A., DUJON B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O68518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTED (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (JUL-1996)
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                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                       WARD M.J., ZUSMAN D.R.;
SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. AF049107; G2947295; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=DZF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRUDEAU K.G., WARD M.J., ZUSMAN D.R.; "Identification and characterization regulator necessary for swarming and MYYDDOCCUS XANTHUS.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DZF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYXOCOCCALES; CYSTOBACTERINEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYXOCOCCUS XANTHUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FY1679;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOL. MICROBIOL. 20:645-655(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myxococcus xanthus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5%;
Local Similarity 27.6%;
es 29; Conservation
                             99
                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLY-PGALLVVDETLLENNPTL-LAVDRAPMTYSIDLPGLASSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMN-YDKKKLLTHOGESIENRFIKEGNQLPDE-FVVIE-RKKRSLSTNTSDISVTATNDS
PLVYISS-VAYGRQVYLKLETTSKSDEVEAAFEALIKGVKVAPQTEWKQI-LDNTEVKAV
                                                                                                                       PLVLVTSDMTFAPKL-LFADPKGRVMEHPYLLATLRSGEELVPPQD-KPIPLPSTG-RLV
                                                                                                                                                                       Similarity 30; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
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                                                                                                                                                                                                                                                                      450 AA;
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                                                                                                                                                                         Conservative
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                                                                                                                                                                                             3.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GENBANK/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 117; DB 3;
Pred. No. 2.32e-02;
28; Mismatches 41
                                                                                                                                                                                             Score 114; DB 2;
Pred. No. 5.91e-02
                                                                                                                                                                         28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                      E3A6FC67 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYXOCOCCACEAE; MYXOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBDIVISION; MYXOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 41;
                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of FrzZ, a novel response fruiting-body formation in
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                                                                                                                                                                            47;
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                                                                                                                                                                                                                    Length 450;
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Best Local
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013705;
01-JAN-1999
01-JAN-1999
01-JAN-1999
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL 95.0 KD PROTEIN C13F5.06C SPAC13F5.06C.
                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TREMBLREL. 01-AUG-1998 (TREMBLREL. 01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                               MEDLINE; 98196666.

DECKERT G., WARRED P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., DECKERT G., WARRED P.V., SNEAD M.A., KELLER M., AUJAY M., HUBER GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;

"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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NATURE 392:353-358(1998).
                             aeolicus
                                                                                                                                                                           STRAIN-VF5
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     BACTERIA;
                                                                                                                                                                                                                                                                                AQUIFEX AEOLICUS
                                                                                                                                                                                                                                                                                                                             DNA GYRASE A SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLLAV-DR-APMTYSIDLPGLASSDSFLQVEDPSNS-SVRGAVNDLLAKWHQDYGQVNNV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IENRFIKEGNQLPDEFVVIERKKRSLSTNTSDISVTATNDSRLYPGALLVVDETLLENNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARMQYEKITAHSM-EQLKVKFGSDFEKTGNSL-DIDFNSVHS-GEK-QIQIVNFKQIYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIVIPFTGVTASSRRETVNI-LSSSISVIECAVNDVFYATVHALGDHLEIILSPYRQISY 670
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Similarity 18.2%;
37; Conservation
                                                                                                                                                                                                                                                   AQUIFICALES;
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(TREMBLREL. 09, LAST SEQUENCE UPDATE)
(TREMBLREL. 09, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                     AQUIFICACEAE;
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07,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 111; DB 3;
Pred. No. 1.48e-01;
70; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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; 6F1C32E5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 84; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  831
                                                                                                                                                                                                                                                                                                                                                                                                                                                              744 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC32;
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Best Local :
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Best Local ;
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058072;

058072;

01-AUG-1998 (TREMBLREL 0

01-AUG-1998 (TREMBLREL 0

01-JAN-1999 (TREMBLREL 0
SEQUENCE FROM N.A
                             ARCHAEA;
                                          PYROCOCCUS HORIKOSHII
                                                                                                                                                                                                                                                                                                                                                                                                     EU ARABIDOPSIS SEQUENCING PROJECT; SUBMITTED (AUG-1998) TO EMBL/GENBA EMBL; ALO31326; E1316763; -. HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TREMBLREL 08, C
01-NOV-1998 (TREMBLREL 08, L
01-NOV-1998 (TREMBLREL 08, L
HYPOTHETICAL 99.2 KD PROTEIN.
F16G20.210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LE GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AE000716; G2983485; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WATSON M.D., GIBBONS T., BARTLEY J., BANCROFT I., MEWES MAYER K.F.X., SCHUELLER C., BEVAN M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPPARALES; BRASSICACEAE; ARABIDOPSIS
                                                                                                                                                                                                                                                              136 QDYGQVNNVPARMQYEKITAHSMEQLKVKFGSDFEKTGNSLDIDFNSVHSGEKQIQIVNF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-VF5;
                                                                                                                                                                                                      196 KQIYYTVSVDAVKNPGDVFQDTV--TVEDLKQR-GISAERPLVYISSVAYG-RQ
                                                                                                                                                                                                                                 332 -PIFYKVKAESVKNQTGHFRNVLLKTEEDVRKKVDRSNIRSILETEDMIWGWRQ 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 KKLVASEGERI-KVFIEETEELVKKYG--D-KRRTFIGGVKEVKEGSITVAVLQDGSIIP 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 VEELPLEKAP-VVNILRVPFT 528
                                                                                                                                                                                                                                                                                                                                Local Similarity nes 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 KKLLTHQGESIENRFIKEGNQLPDEFVVIERKKRSLSTNTSDISVTATNDSRLYPGALLV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 27.28; es 22; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 VDETLLENNPTLLAVDRAPMT
                                                                                                                                                                                                                                                                                    DEY-EIRGRPITTLFERIRESSIA-L-VIFSDKYPESRWCLD-ELVEIKKQMETGSIVPF 331
                                                                         LONG HYPOTHETICAL
                         EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                           867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             744 AA; 84080 MW; 93795328 CRC32;
                                                                                                                                                                                                                                                                                                                             3.3%;
llarity 24.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                     99176 MW; 4847C6E3 CRC32;
                                                                                  07, CREATED)
07, LAST SEQUENCE UPDATE)
09, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                              Pred. No. 26; Misma
                                                                                                                                                                                                                                                                                                                                           Score 110; DB 10;
Pred. No. 2.01e-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 109; DB 2;
Pred. No. 2.71e-01;
23; Mismatches 31
                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                           Mismatches 51;
                                                                                                                                                 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       867 AA.
                                                                                                                                               AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 744;
                                                                                                                                                                                                                                                                                                                                                       Length 867
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PRINCE OCCUPANTE OCCUPANTE
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005541; PREMBLREL 01, CF

01-NOV-1996 (TREMBLREL 01, LF

01-NUC-1998 (TREMBLREL 07, LF

01-AUG-1998 (TREMBLREL 07, LF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O35813 PRELIMINARY;
O35813;
O1-JAN-1998 (TREMBLREL. 05
O1-JAN-1998 (TREMBLREL. 05
O1-NOV-1998 (TREMBLREL. 05
KERATIN 14 (FRAGMENT).
RATTUS NORVEGICUS (RAT).
RUKARYOTA; METAZOA; CHORDZ
                                             SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
                           SACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=ESOPHAGUS;
MEDLINE; 97107478.
WANG D.-Y., XIANG Y.-Y., TANAKA M., SHEN Q., SUGIMURA H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y., YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y., SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCH, AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              esophageal tumors by subtractive cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCIUROGNATHI; MURIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; DNA RES. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=OT3;
MEDLINE; 98344137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 VNNVPARMQY-EKITAHSMEQLKVKFGSD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 IESLTEELAYLKKNHEEEMLALRVRLGGD 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 VDNANVLLQIDNARLA-ANDLRTKYDNETSLRQLVESDINNLRCVLDEL-TMSRADLEMQ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of cytokeratin subspecies altered in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 IEYERQ-YGTLKVIKK----VDNGYELALITEKKIIPVKDWKKV-ENPEIKTRV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 22.5%; nes 20; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 LENNPTLLAVDRAPMTYSIDLPGLASSDSFL-QVEDPSNSSVRGAVNDLLAKWHQDYG-Q 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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D63774; D1023234; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00038; filament; 1.
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Similarity 34.0%;
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231
231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
; 25684 MW;
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                           SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHORDATA; VERTEBRATA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08,05,
                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 104; DB 11;
Pred. No. 1.19e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.19e+
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 6.62e-01; 11; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 106; DB 1;
Pred. No. 6.62e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C908F8E0 CRC32;
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                                                                                                                                                                                                                                                                                                                          303
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SERAIN=S288C (AB972);

FAVELO A., FULTON L., GAITUNG S., GRECO T., KIRSTEN J., KUCABA T.,

FAVELO A., FULTON L., GAITUNG S., GRECO T., KIRSTEN J., KUCABA T.,

PAVELO A., FULTON L., CATRUILES L., JIER M., JOHNSON D.,

NAILSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,

MITLLER N., HANKINS J., HILLIER L., JIER M., JOHNSON D.,

AMILSON R., PAULEY A., PELUSO D., RIFKEN L., RILES L.,

MAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,

AMILSON R., WATERSTON R.;

RISONENCE FROM N.A.

STRAIN=S288C (AB972);

MATERSTON R.;

MATERSTON R.;

MATERSTON R.;
                                                                                                                                                                                                                                          Query Match 3.2%; Score 104; DB 3; Length 303; Best Local Similarity 29.9%; Pred. No. 1.19e+00; Matches 26; Conservative 26; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIL-S288C (AB972);
JIA Y., CHERRY J.M.;
SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U51031; G1332636; -.
SEQUENCE 303 AA; 33964 MW; D494B483 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C (AB972);
FULTON L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (MAY-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                               99 YSIDLPGLASSDSFLQVEDPSNSSVRGAVNDLLAKWHQDYGQVNNVPARMQYE--KI--T 154
                                                                                                                                                                                                      84 YGFELQGLPSKNNMNAGGNGSNSNTNKSMPEPLGHRAQKFILLNNVPHSKNFDDFKILQS 143
                                                                                                                                                                                                                                                   8
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